

us-10-614-524-1.rge

Nov 22 17:22:40 2004

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ORIGIN	Query Match	100.0%;	Score 3687;	DB 6;	Length 3687;				
	Best Local Similarity	100.0%;	Pred. No. 0;						
	Matches 3687;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
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DB	121	ATAGCGAGGGGNAATATATCAATCCACTTGTAGCGCATCAACAGTCCAAACGGGTAT	180						
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DB	241	TTTTATAGTTTTCTTTGTGTGTAATATGCGCCCGCGCGAGAGATCAGTGGGAAATTTTC	300						
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RESULT 2
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LOCUS AR359382 4173 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 37 from patent US 6593293.
ACCESSION AR359382
VERSION AR359382.1 GI:33765692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4173)
AUTHORS Baum, J. A., Chu, C.-R., Donovan, W. P., Gilmer, A. J., and Rupar, M. J.
TITLE Lepidopteran-active Bacillus thuringiensis .delta.-endotoxin
compositions and methods of use
JOURNAL Patent: US 6593293-A 37 15-JUL-2003;
FEATURES
Location/Qualifiers
source 1. 4173
/organism="unknown"
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ORIGIN
Query Match 99.4%; Score 3666.2; DB 6; Length 4173;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3674; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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DEFINITION Sequence 37 from Patent WO0119859.
ACCESSION AX098667
VERSION AX098667.1 GI:13537912
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
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AUTHORS Baum, J. A., Chu, C. R., Donovan, W. P., Gilmer, A. J. and Rupar, M. J.
TITLE Lepidopteran-active bacillus thuringiensis delta-endotoxin
JOURNAL compositions and methods of use
Patent: WO 0119859-A 37 22-MAR-2001;
MONSANTO COMPANY (US)
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ORIGIN		Query Match		99.4%; Score 3666.2; DB 6; Length 4173;	
		Best Local Similarity		99.6%; Pred. No. 0;	
		Matches 3674; Conservative		0; Mismatches 13; Indels 0; Gaps 0;	
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QY	121	ATAGCGGAGGGAATAATATCAATCCACTTTGAGGCAATCAACAGTCCAAACGGGTATT	180		
DB	121	ATAGCGGAGGGAATAATATCAATCCACTTTGAGGCAATCAACAGTCCAAACGGGTATT	180		
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DB	181	AACATAGCTGTAGAAATCTAGGTGTATTAGGCGTACCGTTTCTGCGCAAAATAGCTAGT	240		
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DB	241	TTTTATAGTTTTCTTGTTGGTGAATATATGCGCCCGCGCAGAGATCAAGTGGGAAATTTTC	300		
QY	301	CTAGAACATGTCGAACAACTTATAAATCAACAAATACAGAAATGCTAGGAATAGCGCA	360		
DB	301	CTAGAACATGTCGAACAACTTATAAATCAACAAATACAGAAATGCTAGGAATAGCGCA	360		
QY	361	CTTGCTCGAATACAGGTTTATGAGATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGAT	420		
DB	361	CTTGCTCGAATACAGGTTTATGAGATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGAT	420		
QY	421	TGGCTAGAAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTATACCCAAATATATAGCC	480		
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QY	841	ATAAATACGAGTGTGCTCAGTTAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGG	900		
DB	841	ATAAATACGAGTGTGCTCAGTTAACAGGGAAGTTTATACAGACGCAATTTGAGCAACAGG	900		
QY	901	GTAATATGCAAGTATGAATTTGGTATAATAATATGCACTTCTGTTTTCGGCTTATAGAG	960		
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DB	1021	ACTTCATCAAGATGGAGTCTAGGCATATGACTTACTTGGCGGGGCGACAAATTCAA	1080		
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DB	1141	AATCCTGTGAAGATTAATCTTCTCTCGAGACGCTATATTGGACTGAATCATATGCGAG	1200		
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DB	1201	GTGCTTCTATGGGGAATTTACCTTGAACCTTATCATGGTCTCTTCTAGATTTAAT	1260		
QY	1261	TTTAGGAACCTCTCAGATATCTTTTGAAGAGGTAATGCTTAACATATAGTCAACCTTATG	1320		
DB	1261	TTTAGGAACCTCTCAGATATCTTTTGAAGAGGTAATGCTTAACATATAGTCAACCTTATG	1320		
QY	1321	TCACCTGGGCTTCAATTTAAAGATTCAGAACTGAAATTTACCAACCAACAGACGA	1380		
DB	1321	TCACCTGGGCTTCAATTTAAAGATTCAGAACTGAAATTTACCAACCAACAGACGA	1380		
QY	1381	CGAAATATGATATCATATAGTATAGTATCTCAGATAGGCTCATTTTCAAAATCTAGG	1440		
DB	1381	CGAAATATGATATCATATAGTATAGTATCTCAGATAGGCTCATTTTCAAAATCTAGG	1440		
QY	1441	GTGCTATGACAGTATATTTTGGACGCGATGATGCGATGCTAGACAAATACCATTTAGT	1500		
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RESULT 4
AF077326 3684 bp DNA linear BCT 26-AUG-1998
LOCUS AF077326
DEFINITION Bacillus thuringiensis CryI_{BeI} delta-endotoxin gene, complete cds.
ACCESSION AF077326
VERSION AF077326.1 GI:3360518
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3684)
Payne, J., Cummings, D. A., Cannon, R. J. C., Narva, K. E. and Stelman, S. J.
Bacillus thuringiensis genes encoding lepidopteran-active toxins
Patent: US 5723758 03-MAR-1998;
Mycogen Corporation; San Diego, CA
REFERENCE 2 (bases 1 to 3684)
Stelman, S. J.
Direct Submission
Submitted (08-JUL-1998) Molecular Biology, Mycogen Corporation,
5501 Oberlin Dr., San Diego, CA 92121, USA
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190319
LOCUS
DEFINITION Sequence 7 from patent US 5723758.
ACCESSION 190319
VERSION 190319.1 GI:3410259
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3684)
AUTHORS Payne, J., Cummings, D. A., Cannon, R. J. C., Narva, K. E. and Steiman, S.
TITLE Bacillus thuringiensis genes encoding lepidopteran-active toxins
JOURNAL Patent: US 5723758-A 7 03-MAR-1998;
FEATURES Location/Qualifiers

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DEFINITION AR359400
ACCESSION AR359400
VERSION AR359400.1 GI:33765710
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCES 1 (bases 1 to 3684)
AUTHORS Baum, J. A., Chu, C.-R., Donovan, W. P., Gilmer, A. J. and Rupar, M. J.
TITLE Lepidopteran-active Bacillus thuringiensis .delta.-endotoxin
JOURNAL compositions and methods of use
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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1 Baum, J.A., Chu, C.R., Donovan, W.P., Gilmer, A.J. and Rupar, M.J.
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ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3687)
AUTHORS Brizzard,B.L. and Whiteley,H.R.
TITLE Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis
JOURNAL Nucleic Acids Res. 16 (6), 2723-2724 (1988)
MEDLINE 88203216
PUBMED 3362680
REFERENCE 2 (bases 1 to 3687)
AUTHORS Whiteley,H.R.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1988) Whiteley H. R., Department of W, Department of Microbiology, University of Washington, Seattle, WA 98195
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ORIGIN

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DEFINITION Bacillus thuringiensis plasmid encoded CryIbA (cryIbA) gene,
complete cds.
ACCESSION AF368257
VERSION AF368257.1 GI:14486713
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ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE 1 (bases 1 to 3687)
AUTHORS Zhang, J., Song, F. and Huang, D.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2001) Biotechnology Research Group, IPP, CAAS, 2
West Yuanningyuan Road, Beijing, China
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Query Match 85.0%; Score 3135.2; DB 1; Length 3687;
Best Local Similarity 91.1%; Pred. No. 0;
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ORIGIN

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QY	1021	ACTTCATACGATGAGTCTACTAGGCATATGACTTCTGCGGGGGGACACAAATTCAA	1080
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Db	1126	AATCCTGTAAAGATTATCATTTCTCTCGAGACGTATATTTGGACTGAATCATATCGAGA	1185
QY	1201	GTGCTTCTATGGGAATTTTACCTTGAACCTATTTATGTTGTCCTTACTGTTAGATTTAAT	1260
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QY	1261	TTTAGGAACCTTCAGATACTTTTGAAGAGGTACTGCTTAATCTATAGTCAACCTTATGAG	1320
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QY	1321	TCACCTGGGCTTCAATTTAAAAGATTTCAGAAATGAAATTCACCAAGAAACCAAGAA	1380
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QY	1441	GTGCAATGACCAAGTATATTTTGGACCGCAGTGTAGTCAGATCGTACAAATACCAATAGT	1500
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QY	1561	GTAGTCAGTGGCCCGAGGATTTACAGGAGGGGATATAATTCGAACTAACGGTTAATGGTAGT	1620
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QY	1621	GTACTAAGTATGGGTCTTAATTTTAAATTAATACATCATTTACAGCGGTATCGGTGAGAGTT	1680
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Qy	2278	GAAGGAATGACGTATTTAAAGAGAAATTAAGTGCACACTACCGGGACCTTTAATGAGTGT	2337
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Qy	2338	TATCCGACGTATTTATATCAAAAAATAGGAGAGTCCGAAATTTAAAGGCTTATACTCGCTAC	2397
Db	2326	TATCCGACGTATTTATATCAAAAAATAGGAGAGTCCGAAATTTAAAGGCTTATACTCGCTAC	2385
Qy	2398	CAATTAAGAGGGTTATATGGAAGTAGTCAAGATTTAGAGATATATTTGATTCGTTATAAT	2457
Db	2386	CAATTAAGAGGGTTATATGGAAGTAGTCAAGATTTAGAGATATATTTGATTCGTTATAAT	2445
Qy	2458	GCGAAAACATGAAACATTTGGAATGTTCCAGGTACCGAGTCCCGTATGGCCGCTTTTCAGTTGAA	2517
Db	2446	GCGAAAACATGAAACATTTGGAATGTTCCAGGTACCGAGTCCCGTATGGCCGCTTTTCAGTTGAA	2505
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Qy	3358	GATACAGGAACGTGTATATGATATATCTGCACACCCAGGTACAGC-----AGTA	3405
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Qy	3466	AATTACAAACCGACTTATGAAGAGAAACGTTATACAGATGTACGAAGAGATATCATTTGT	3525
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Qy	3586	TTAGATATCTCCAGAAACCGATAGGTATGAGATGAGATGAGAGAAACGGAAGGAAG	3645
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4074 bp

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PAT 07-OCT-1997

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DEFINITION	Sequence 1 from patent US 5628995.
ACCESSION	I42103
VERSION	I42103.1 GI:2467598
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
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AUTHORS	Peferoen,M., Janssens,S. and Denolf,P.
TITLE	Control of Oestrinia
JOURNAL	Patent: US 5628995-A 1 13-MAY-1997;
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QY	421 TGGCTAGAAACCGTGATGTCGAAGAACGAGAAGTGTCTTTATACCAATATATAGCC 480
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QY	481 TTAGAACTTGATTTTCTTAATGCGATGCCCTTTTTCGAATTAAGAAACCAAGAGTTCCA 540
Db	651 TTAGAACTTGATTTTCTTAATGCGATGCCCTTTTTCGAATTAAGAAACCAAGAGTTCCA 710
QY	541 TTATTATGTTATATGCTCAAGCTGCNAATTTACACTTATTATTAGAGATGCTCT 600
Db	711 TTATTATGTTATATGCTCAAGCTGCNAATTTACACTTATTATTAGAGATGCTCT 770
QY	601 CTTTTTGGTAGTGAATTTGGGCTTACATCGAGGAAATTCACGGTTATTATGAGCGCCA 660
Db	771 CTTTTTGGTAGTGAATTTGGGCTTACATCGAGGAAATTCACGGTTATTATGAGCGCCA 830
QY	661 GTGGAACAAACGAGAGATTATCCGACTATTGCGTAGAATGGTATAATAACAGGCTTAAT 720
Db	831 GTGGAACAAACGAGAGATTATCCGACTATTGCGTAGAATGGTATAATAACAGGCTTAAT 890
QY	721 AGCTTGAGAGGGAACAAATCCGCAAGTTCGGTGGTATTAAATCAATTCGGTAGAGATCTA 780
Db	891 AGCTTGAGAGGGAACAAATCCGCAAGTTCGGTGGTATTAAATCAATTCGGTAGAGATCTA 950
QY	781 ACGTTAGGGGTATTAGATCTAGTGGCACTATCCCAAGCTATGACACTCGCACTTATCCA 840
Db	951 ACGTTAGGGGTATTAGATCTAGTGGCACTATCCCAAGCTATGACACTCGCACTTATCCA 1010
QY	841 ATAAATACGAGTGTCTCAGTTTAAACAGGGAGTTTATACAGACCAATTTGAGCAACAGGG 900
Db	1011 ATAAATACGAGTGTCTCAGTTTAAACAGGGAGTTTATACAGACCAATTTGAGCAACAGGG 1070
QY	901 GTAATATGCAAGTATGAATTTGGTATAATAATAATGACACTTCGTTTCCGCTATAGAG 960
Db	1071 GTAATATGCAAGTATGAATTTGGTATAATAATAATGACACTTCGTTTCCGCTATAGAG 1130
QY	961 ACTGCGTTATCCGAAGCCGCACTACTTCTCTCGAGACGTATATTGGACTGAATCATATCGAGA 1020
Db	1131 GCTGCGGTATCCGAAGCCGCACTACTTCTCTCGAGACGTATATTGGACTGAATCATATCGAGA 1190
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Db	1191 GCTTCATACGATGGAGTGTCTACTAGGCATATGACTTACTGCGGGGGCACAAATTCAA 1250
QY	1081 TCTCGGCCAATAGGAGGCGGATTAATACCTCAACGATGGGTCTACCAATACTTCTATT 1140
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QY	1141 AATCTCTGAAGATTATCACTTCTCTCGAGACGTATATTGGACTGAATCATATCGAGA 1200
Db	1311 AATCTCTGAAGATTATCACTTCTCTCGAGACGTATATTGGACTGAATCATATCGAGA 1370
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Db	1371 GTGCTTCTATGGGGAATTTTAACTTGAACCTATTCTATGGTGTCCCTTACTGTTAGATTTAAT 1430
QY	1261 TTTTAGAACCCCTCAGATACCTTTTGGAGAGGTACTGCTAACTATAGTCAACCCCTATGAG 1320
Db	1431 TTTTAGAACCCCTCAGATACCTTTTGGAGAGGTACTGCTAACTATAGTCAACCCCTATGAG 1490
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QY	1621 GTACTAGTATGGTCTTAAATTTTAAATACATCATTTACAGCGGTATCCGCTGAGAGTT 1680
Db	1791 TTTGGACCGAATAAGAGTAACCTGTAAACGGACCAATTAACACAAAGATATCGTAGGATTC 1850
QY	1681 CGTTATGCTGCTTCTCAAAACAAATGGTCTCGAGGTAACTGTCCGAGGAGTACTACTTTT 1740
Db	1851 CGCTATGCTTCAACTGTAGATTTTGAATTTCTTTGTATCAGTGGAGGTACTACTGTAAT 1910
QY	1741 GATCAAGATTCCCTAGTACTATGATGCAAAATGAGTCTTTTGACATCTCAATCATTTAGA 1800
Db	1911 AATTTTAGATTCTCATCGTACCAATGAACAGTGGAGACGAATAAAATACGGAAATTTTGTG 1970
QY	1801 TTTTGCAAGATTTCTCTAGGTATTAGTCATCTGGCAGGTCAA---ACTGCTGGAATAAGT 1857
Db	1971 AGACGTGCTTTTACTACACCTTTTACTTTTACAAATTTCAAGATATAATTCGAACGTCT 2030
QY	1858 ATAAGTAATAATGCGAGGTAGACAAACGTTTTCATCTTTGATAAAATTTGAATTTCAATTC 1917

Db	2031	ATTCAAGGCCTTAGTGGAAATGGGGAAGTGTATATAGATAAAATTGAAATATTTCAGATT	2090
Qy	1918	ACTGCAACCTTTCGAAGCAGAAATCCGATTTAGAAAGGGCGCAGAGGGCGGTGAATGCTCTG	1977
Db	2091	ACTGCAACCTTCGAAGCAGAAATGATTTAGAAAGAGCGCAGAGGGCGGTGAATGCTCTG	2150
Qy	1978	TTTACTAATACGAATCCAGAGATTGAAACAGATGTGACAGATTATCATATTGATCAA	2037
Db	2151	TTTACTAATACGAATCCAGAGATTGAAACAGATGTGACAGATTATCATATTGATCAA	2210
Qy	2038	GTATCCAAATTTAGTGGCGTGTATCCGATGAATTTCTGCTTAGNTGAAAGAGAGAATTA	2097
Db	2211	GTATCCAAATTTAGTGGCGTGTATCCGATGAATTTCTGCTTAGNTGAAAGAGAGAATTA	2270
Qy	2098	CTTGAGAAAGTGAATATGCGAAACCACTCAGTGTAGTGAAGAAACCTTACTCCAGATCCA	2157
Db	2271	CTTGAGAAAGTGAATATGCGAAACCACTCAGTGTAGTGAAGAAACCTTACTCCAGATCCA	2330
Qy	2158	AACCTTCACATCCATCAATAAGCAACCAAGCTTCATATCTACTAATGAGCAATCGAATTTTC	2217
Db	2331	AACCTTCACATCCATCAATAAGCAACCAAGCTTCATATCTACTAATGAGCAATCGAATTTTC	2390
Qy	2218	ACATCTATCCATGAAACCAATCTGAAACCACTGATGGGGAAGTGAGAACATTAACAATCCAG	2277
Db	2391	ACATCTATCCATGAAACCAATCTGAAACCACTGATGGGGAAGTGAGAACATTAACAATCCAG	2450
Qy	2278	GAAGGAATGACGTATTTAAAGAGAATTACGTGCACACTACCGGGGACTTTTAAATGAGTGT	2337
Db	2451	GAAGGAATGACGTATTTAAAGAGAATTACGTGCACACTACCGGGGACTTTTAAATGAGTGT	2510
Qy	2338	TATCCGACGTATTTATATCAAAAAATAGGAGAGTCCGAATTTAAAGCTTATATCTCCTAC	2397
Db	2511	TATCCGACGTATTTATATCAAAAAATAGGAGAGTCCGAATTTAAAGCTTATATCTCCTAC	2570
Qy	2398	CAATTAGAGGGTATATTGAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAT	2457
Db	2571	CAATTAGAGGGTATATTGAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAT	2630
Qy	2458	GGCAAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGTATGGCGGCTTTTCAGTTGAA	2517
Db	2631	GGCAAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGTATGGCGGCTTTTCAGTTGAA	2690
Qy	2518	AGGCCAATCGGAAGGTGCGGAGAACCGAATCGATGGCACCAATTTGGAATGGAATCCCT	2577
Db	2691	AGGCCAATCGGAAGGTGCGGAGAACCGAATCGATGGCACCAATTTGGAATGGAATCCCT	2750
Qy	2578	GATCTAGATTGTTCCCTCGAGAGATGGAGAAAAATGCGCGCATCATTCGCATCATTTCTCT	2637
Db	2751	GATCTAGATTGTTCCCTCGAGAGATGGAGAAAAATGCGCGCATCATTTCCCATCATTTCTCT	2810
Qy	2638	TTGGATATTCGATATTGGATGCACAGACTTCGATGAGAAATCTAGCGGTGTGGGTGGTATTC	2697
Db	2811	TTGGATATTCGATATTGGATGCACAGACTTCGATGAGAAATCTAGCGGTGTGGGTGGTATTC	2870
Qy	2698	AAGATTAAAGCGCAGGAAGTCTATGCAAGACTAGGGAATCTGGAAATTTATTGAAGAGAAA	2757
Db	2871	AAGATTAAAGCGCAGGAAGTCTATGCAAGACTAGGGAATCTGGAAATTTATTGAAGAGAAA	2930
Qy	2758	CCATTATTAGGAGAGACACTGTCTGTGTGAGAGAGCAGAGAAAAAATTTGGAGAGACAAA	2817
Db	2931	CCATTATTAGGAGAGACACTGTCTGTGTGAGAGAGCAGAGAAAAAATTTGGAGAGACAAA	2990
Qy	2818	CGTGAAAAAATACAAATTTGGAAAAAACAACAGAGTATATACAGAGCCAAAGAGCTGTGGAT	2877
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Qy	2878	GCCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATGATT	2937
Db	3051	GCCTTTATTTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATGATT	3110
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Qy	2998	ATCCCGGGTGTAAATGCGGAAATTTTTTGAAGAAATTAGAAGGTCGCAATTAATCACTGCGCAATC	3057
Db	3171	ATCCAGGTGTAAATGCGGAAATTTTTTGAAGAAATTAGAAGGTCACATTAATCACTGCGCAATC	3230
Qy	3058	TCCCTATACGATGCGGAGAAATGTCGTTTAAATAATGTTGTAATTTTAATTAATGGAATTAGCATGC	3117
Db	3231	TCCTTATACGATGCGGAGAAATGTCGTTTAAATAATGTTGTAATTTTAATTAATGGAATTAAACATGT	3290
Qy	3118	TGGAATGTAAAGGGCAGTGTAGATGTATCAACAGAGCCATCACCGTTCGTGCTGCTGTTGTTATC	3177
Db	3291	TGGAATGTAAAGGGCAGTGTAGATGTATCAACAGAGCCATCATCGTTCGACCTTGTGTTATC	3350
Qy	3178	CCAGAAATGGGAAGCAGAAAGTGTACAAAGCAGTTCGCGTCTGTCCGGGGCGTGCCTATATC	3237
Db	3351	CCAGAAATGGGAAGCAGAAAGTGTACAAAGCAGTTCGCGTCTGTCCGGGGCGTGCCTATATC	3410
Qy	3238	CTCCGTGTCAACGGGTACAAAGAGGAGTATGAGAGAGGTTGTGTAAACGATCCCATGAATC	3297
Db	3411	CTTCGTGTCAACGGGTACAAAGAGGAGTATGAGAGAGGTCGCTTAACGATCCCATGAATC	3470
Qy	3298	GAGAACAAATACAGACGAACTAAATTTTAAATACTGTGAAAGAGGAGTATCCCAACG	3357
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Qy	3358	GATACAGAAACGTGTAAATGATTAATCTGCACACCAAGGTACAGC-----AGTA	3405
Db	3531	GATACAGAAACGTGTAAATGATTAATCTGCACACCAAGGTACAGC-----AGTA	3590
Qy	3406	TGTAAATCCCGTAAATGCTGGATATGAGGATGCAATATGAAGTTGATATACAGCATCTGTT	3465
Db	3591	TGTAAATCCCGTAAATGCTGGATATGAGGATGCAATATGAAGTTGATATACAGCATCTGTT	3650
Qy	3466	AATTACAAACCGACTTATGAAGAGAAACGTTATACAGATGCTACGAAGAGATATCATTTGT	3525
Db	3651	AATTACAAACCGACTTATGAAGAGAAACGTTATACAGATGCTACGAAGAGATATCATTTGT	3710
Qy	3526	GAATATACAGAGGGTATGTGAATTAATCCACCACTACCAGCTCGTTTATATGACAAAGAA	3585
Db	3711	GAATATACAGAGGGTATGTGAATTAATCCACCACTACCAGCTCGTTTATATGACAAAGAA	3770
Qy	3586	TTAGAATACATCCAGAAACCGATAAGTATGAGATTGAGATTGCGAGAAACGGAAGGGAAG	3645
Db	3771	TTAGAATACATCCAGAAACCGATAAGTATGAGATTGAGATTGCGAGAAACGGAAGGGAAG	3830
Qy	3646	TTTATTGTACAGCGTGGAAATTTACTCCTTATGAGAGGAATAG	3687
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AF363025			
LOCUS			
DEFINITION			
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VERSION			
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RESULT 13
BACCRYIE 3934 bp DNA linear BCT 25-APR-1994
LOCUS Bacillus thuringiensis crystal protein (cryI E75) gene, complete
DEFINITION cde.
ACCESSION L32020.1 GI:474893
VERSION crystal protein.
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3934)
AUTHORS Donovan, W.P.
JOURNAL Unpublished (1994)
COMMENT Original source text: Bacillus thuringiensis (strain EG 5847) DNA.
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TWIEIGETEGKEFVDSVBLELME"

ORIGIN

Query Match 72.9%; Score 2687.2; DB 1; Length 3934;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 3088; Conservative 593; Indels 15; Gaps 3;
QY 1 TTGACTTCAATAGGAAATGAGATGAAATTAATTAATGCTTTATCGAATCCAGCTGTA 60
Db 67 TTGACTTCAATAGGAAATGAGATGAAATTAATTAATGCTTTATCGAATCCACGTA 126

QY 61 TCGAATCAATCCACACAAATGGATCTATCACCAGATGCTCGTATTGAGGATCTTTGTGT 120
Db 127 TCGAATCTTTCCACGCAATGAATCTATCACCAGATGCTCGTATTGAGGATCTTTGTGT 186
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Db <td>3421</td> <td>CCAAACGGATACAGGAACGTGTAACTATTATCTGCACACCAAGGTACAGCAGTATGTAAAT</td> <td>3480</td>	3421	CCAAACGGATACAGGAACGTGTAACTATTATCTGCACACCAAGGTACAGCAGTATGTAAAT	3480
Qy <td>3412</td> <td>TCCCGTAATGCTGGGATATGAGGATGCAATATGAAGTTGATCTACAGCATCTGTTAAATTAC</td> <td>3471</td>	3412	TCCCGTAATGCTGGGATATGAGGATGCAATATGAAGTTGATCTACAGCATCTGTTAAATTAC	3471
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ACCESSION	AR068828		
VERSION	AR068828.1	GI:6001035	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 3934)		
AUTHORS	Donovan, W.P. and Gonzalez, J.M. Jr.		
TITLE	Bacillus thuringiensis bacterina		
JOURNAL	Patent: US 5854053-A 3 29-DEC-1998;		
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Best Local Similarity	83.5%;	Pred. No. 0;	
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Qy	181	ACATAGCTGGTAGAATATCTAGTGTATPAGCGTACCGTTTGTCTGGACAAATAGCTAGT	240
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ACCESSION I38760
VERSION I38760.1 GI:2083238
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3934)
AUTHORS Donovan, W.P., Tan, Y., Jany, C.S. and Gonz alez, Je.M. Jr.
TITLE Bacillus thuringiensis cryET5 gene and related plasmids, bacteria
and insecticides
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Query Match 72.9%; Score 2687.2; DB 6; Length 3934;
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Db 127 TCGAATCCTTCCACCAATGAAATCTATCACAGATGCTGCTATTTAGAGATTCCTTTGTGT 186
QY 121 ATAGCGGAGGGGATAATATCAATCCACTTGTAGCGCATCAACAGTCCAAACGGGTATT 180
Db 187 GTAGCGGAGGGTGAACAATATTGATCCATTTGTAGCGCATCAACAGTCCAAACGGGTATA 246
QY 181 AACATAGCTGTAGAACTACTAGGTGATATAGCGGTACCGTTCGTGGAACAATAGCTAGT 240
Db 247 AACATAGCTGTAGAACTACTAGGTGATATAGCGGTACCGTTCGTGGAACAATAGCTAGT 306
QY 241 TTTTATAGTTTCTTGTGTGTAATTATGGCCCGCGGACAGATCAGTGGGAAATTTTC 300
Db 307 TTTTATAGTTTCTTGTGTGGAATTATGGCCCTAGTGGCAGAGATCCATGGGAAATTTTC 366
QY 301 CTAGAACATGTCGAACAACCTTATTAATCAACAATAACAGAAATGCTAGGAATACGGCA 360
Db 367 CTGGAACATGTAGNAACCTTATAGCAACAAGTAAACAGAAATACTAGGAATACGGCT 426
QY 361 CTGCTCGATTACAAGTTTAGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Db 427 ATTGCTCGATTAGAAAGTCTAGGAAGGCTATAGATCTTACACGAGGCTCTTGAAGT 486
QY 421 TGGCTAGAAAACCGTGTATGATGCAAGACGAGAGTTCCTTTATACCCAAATATAGCC 480
Db 487 TGGTATAGTAACCGAAATGATCGAGATCAAGAAGCATTAATCTTGGAGCGCTATGTTCT 546
QY 481 TTAGAACTGGATTTCTTAATGCGATGCGCGCTTTTCGCAATTAGAAACCAAGAGTTCCT 540
Db 547 TTAGAACTTTGACATTACTACTGCTATACCGCTTTTTCAGATACGAAATGAAGAAGTTCCT 606
QY 541 TTATTAAATGGTATATGCTCAAGCTGCAATTTACCTATTATTATTGAGAGATGCGCTCT 600
Db 607 TTATTAAATGGTATATGCTCAAGCTGCAATTTTACACCTATTATTATTGAGAGATGCGCTCT 666
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QY 601 CTTTTTGTAGTGAATTTGGCTTACATCGCAGGAAATTCACGTTATTATGACGCGCAA 660
Db 667 CTTTTTGTAGTGAATTTGGGATGGCATCTCCGATGTTAACNATATTATCAAGAACAA 726
QY 661 GTGGAACAAACGAGAGATTTTCGACTATTTGGGTAGAATGGTATATATACAGGTCTTAAT 720
Db 727 ATCAGATATACAGAGGAATATTCTAACCATTTGGGTACAATGGTATATAATACAGGGCTAAAT 786
QY 721 AGCTTGAGAGGACAAATGCGCAAGTTGGGTGCGTTATTAATCAATTCGTTAGAGATCTTA 780
Db 787 AACTTAAGAGGACAAATGCTGAAAGTTGGTTCGGGTATTAATCAATTCGTTAGAGACCTTA 846
QY 781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGATACTCGCACTTATCCA 840
Db 847 ACGTTAGGGGTATTAGATTTAGTAGCCCTATTCCCAAGCTATGATACTCGCACTTATCCA 906
QY 841 ATAAATACGAGTCTCAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGG 900
Db 907 ATCAATACGAGTCTCAGTTTAAACAGAGAAATTTATACAGATCCCAATTTGGGAGAACAAAT 966
QY 901 GTAAAT-----ATGCGCAAGTATGAATTTGGTATATAATAATGCACCTTCGTTTCCGCT 954
Db 967 GCACCTTCAGGATTTGCAAGTACGAATTTGGTTTAATAATAATGCACCATCGTTTCTGCC 1026
QY 955 ATAGAGACTGCGGTTTATCCGAAGCCCGCATCTACTTTGATTTTCTAGAACAACTTACAATT 1014
Db 1027 ATAGAGGCTGCCATTTTCAGGCCCTCCGCACTACTTTGATTTTCCAGAACAACTTACAATT 1086
QY 1015 TTTAGCATTTCATCAGATGAGTCTCTAGGCAATATGACTTACTTGGCGGGGACACACA 1074
Db 1087 TACAGTGCATCAAGCGGTTGGAGTAGCACTCAACATATGAATTTATGGTGGGACATAGG 1146
QY 1075 ATTCAATCTCGGCCAATAGGAGCGGATTAATAATACCTCAACGCAATGGTCTACCA---AT 1131
Db 1147 CTTAACTTCCGCCCAATAGGAGGACATTAATACTCAACACAAAGGACTTACTATAAT 1206
QY 1132 ACTTCTATTAATCTGTGAAGATTAATCTTCTCTCGAGACGTATATTTGGACTGGAATCA 1191
Db 1207 ACTTCAATTAATCTGTGAACATTAACAGTTACGTTACGTTCTCGAGCGTTTATAGACAGATCA 1266
QY 1192 TATGAGAGTGTCTTCTATGGGAAATTTACCTTGAACCTATTCATGGTGTCCCTACTGTT 1251
Db 1267 AATGACGGGACAAATAT-----ACTAATTTACTCTCTGTGAATGGAGTACCTTGGGCT 1320
QY 1252 AGATTTAATTTTAGGAACCTCTCAGAACTATTTTGAAGAGGTACTGCTAACTATAGTCAA 1311
Db 1321 AGATTTAATTTTATAAACCCCTCAGAAATATTATGAAGAGGCGCCACTACCTACACTCAA 1380
QY 1312 CCCTATCAGTCACTGGGCTTCAATTTAAAGATTTACAGAACTGAAATTAACCCAGAAACA 1371
Db 1381 CCGTATCAGGGAGTTGGGATTCANTTATTGATTTCAGAACTGAAATTAACCCAGAAACA 1440
QY 1372 ACAGAACGACCAATTTATGAATCATATAGTCAATAGTATTCTCAGATAGGCTCATTTCA 1431
Db 1441 ACAGAACGACCAATTTATGAATCATATAGTCAATAGTATTCTCAGATAGGCTCATTTCA 1500
QY 1432 CAATCTAGGTCATCTACAGTATATCTTCGAGCGCCGCTAGTGCAGATCGTACAAAT 1491
Db 1501 GGAACACACTTTGAGACACCACTCTATTCTTGGACGATCGTAGTGCAGATCGTACGAAT 1560
QY 1492 ACCATTTAGTTTCAGATAGCATACACAAATACCATTTGGTAAATCAATCAACCTTAATTTCA 1551
Db 1561 ACATTTGGACCAATTAAGAAATTAACAAATACCATTTGGTAAAGCACTGAATCTTCATTTCA 1620
QY 1552 GGTACCTCTGTAGTCAGTGGCCCGAGATTTACAGGAGGGGATATAATCCGAACTAAAGTT 1611
Db 1621 GGTGTTACTTGTGTTGGAGGCGCAGATTTACAGTGGGGATATCCTTCGTAGAACAAAT 1680
QY 1612 AATGCTAGTGTACTAAGTATGGGTCTTAATTTTAAATATATCATATTAACAGCGGTATCGC 1671
Db 1681 ACGGGTACATTTGGAGATATACGATTAATAATTAATGTGCCATTTATCCCAAGATATCGC 1740
QY 1672 GTGAGAGTTCGTTATGCTGCTTCTCAACAAATGCTGCTGAGGGTAACTGTGCGGAGGAGT 1731
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Db 1741 GTAAAGGATTCGTATGCTCTCTACTACAGATTTTCAAAATTTTTCACGAGAAATTAATGGAACC 1800
Qy 1732 ACTACTTTTGGATCAAGGATTCCTAGTACTATGAGTGCAAAATGAGTCTTTTGACATCTCAA 1791
Db 1801 ACTGTTAATATTTGGTAAATTTCTCAAGAACTATGAATAGGGGGGTAATTTTAGAATATAGA 1860
Qy 1792 TCATTTAGATTTGCGAAGATTTCTCTGAGGTATTTAGTGCAATCTGGCAGTCAAACTCTCGGA 1851
Db 1861 AGTTTTAGAACTGCGAGGATTTAGTACTCTCTTTTAAATTTTAAATGTCCTCAAGCAATTC 1920
Qy 1852 ATAAGTATAAGTAATAATCGAGGTAGACAAAGCTTTTCACTTTGATAAATAATGCAATTCAT 1911
Db 1921 ACAATGGGGTCTCAGAGTTTTTCAATCAGGAAGTTTATATAGATAGAGTCGAATTTGTT 1980
Qy 1912 CCAATTTACTGCAACCTTGAAGCAGAAATACGATTTTAGAAAGGGCGCAGAGGCGGTGAAT 1971
Db 1981 CCAGCAGAGGTAAACATTTGAGCGAGATATGATTTTAGAAAGAGCAAAAGGCGGTGAAT 2040
Qy 1972 GCTCTGTTTACTAATACGAATCCAAAGAGATTTGAAACACAGATGTGACAGATTTATCATATT 2031
Db 2041 GCTCTGTTTACTTCTACAAATCCAAAGAGATTTGAAACACAGATGTGACAGATTTATCATATT 2100
Qy 2032 GATCAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGCTTTAGATGAAGAGAGA 2091
Db 2101 GACCAAGTGTCCAATATGCTGGCATGTTTATCAGATGAATTTTGTCTTGATGAGAAGGGA 2160
Qy 2092 GAATTTACTTTGAGAAAGTGAATATCGAAACGACTCAGTGATGAAGAACTTTACTCCAA 2151
Db 2161 GAATTTTGGAAAGTGAATATCGGAAGCGACTCAGTGATGAAGAACTTTACTCCAA 2220
Qy 2152 GATCCAAACTTCCATCCATCAATGAAGCAACAGACTTTCATATCTACTAATGAGCAATCG 2211
Db 2221 GATCCAAACTTCCATCCATCAAGTGGCAATTTAAGTTTCGCATCCATCGATGGAACAATCA 2280
Qy 2212 AATTTCAATCTATCCATGAACAACTCTGAACTAGATGTTGGGGAAGTGAGAACTATACA 2271
Db 2281 AACTTCCCTCTATTAATGAGCTATCTGAACATGATGTTGGGGAAGTGCGAATGTTTACC 2340
Qy 2272 ATCCAGGAAGGAATAGCTATTTTAAAGAAATTAAGTACACTACCGGGGACTTTTAAAT 2331
Db 2341 ATTCAAGGAAGGAATGAGCTATTTTAAAGAAATTAAGTACACTACCGGGGACTTTTAAAT 2400
Qy 2332 GAGTGTATCCGAGTATTTATATCAAAATPAGGAGAGTTCGGAATTTAAAGCTTTATACT 2391
Db 2401 GAGTGTATCCAAATTTATATCAAAATPAGGAGAGTTCGGAATTTAAAGCTTTATAGC 2460
Qy 2392 CGCTACCAATTAAGAGGTATATTTGAAGATAGTCAAGATTTTAGAGATATATTTGATTCGT 2451
Db 2461 CGCTATCAATTAAGAGGTATATTTGAAGATAGTCAAGATTTTAGAGATTTATTTAATTCGT 2520
Qy 2452 TATATATGCAACATGAAACATTTGATGTTCCAGGTACCGAGTCCGATGCGCGCTTCA 2511
Db 2521 TACAATGCAAGCATGAAACATTTGATGTTCCAGGTACCGAGTCCGATGCGCGCTTCA 2580
Qy 2512 GTTGAAGCCCAATCGGAAGTTCGGAGAACCGAATCGATGCGCACCACTTTTGAATGG 2571
Db 2581 GTTGAAGCCCAATCGGAAGTTCGGAGAACCGAATCGATGCGCACCACTTTTGAATGG 2640
Qy 2572 AATCTGATCTAGATTTGTTCTGCAAGATGGAAGAAATGTCGCATCATTTCCCATCAT 2631
Db 2641 AATCTGATCTAGATTTGTTCTGCAAGATGGAAGAAATGTCGCATCATTTCCCATCAT 2700
Qy 2632 TTCTCTTTGGATTTGATTTGATTTGATGTCAGACTTTCGATGAATCTAGGCGTGGGGTG 2691
Db 2701 TTCTCTTTGGATTTGATTTGATTTGATGTCAGACTTTCGATGAATCTAGGCGTGGGGTG 2760
Qy 2692 GTATTTCAAGATTTAAGACGAGGAAGCTCATGCAAGACTAGGGAATCTGGAATTTTATGAA 2751
Db 2761 GTATTTCAAGATTTAAGACGAGGAAGCTCATGCAAGATTTAGGAATCTGGAATTTATCGAA 2820
Qy 2752 GAGAAACCAATTTATAGGAAGCACTGCTCTGTTGAAAGAGAGCAAGAAATGGAAG 2811

Db 2821 GAGAAACCAATTTATTTGGAGAGCACTGCTCGTGTGAAGAGAGCGGAAAAAATTTGGAGA 2880
Qy 2812 GACAAACGTAAGAACTACAAATTTGAAACAAAACGAGTATATACAGAGCAAAAGAGCT 2871
Db 2881 GACAAACGTAAGAACTACAAATTTGAAACAAAACGAGTATATACAGAGCAAAAGAGCT 2940
Qy 2872 GTGGATGCTTTATTTGTAGATTTCTCAATATATATAGATTTCAAGCGGATACAAACATTTGC 2931
Db 2941 GTGGATGCTTTATTTGTAGATTTCTCAATATATATAGATTTCAAGCGGATACAAACATTTGC 3000
Qy 2932 ATGATTCATGCGGCGAGATAAACTTTGTTTCATCGAATTCGAGAGGCTTATCTGTGAGATTA 2991
Db 3001 ATGATTCATGCGGCGAGATAAACTTTGTTTCATCGAATTCGAGAGGCTTATCTTTTCAGAA 3060
Qy 2992 TCTGTTATCCCGGGTGTAAATGCGGAAATTTTGAAGAAATTTGAAGGTCGCAATTTCACT 3051
Db 3061 CTTGTTATCCAGAGTGTAAATGCGGAAATTTTGAAGAAATTTGAAGGTCGCAATTTCACT 3120
Qy 3052 GCAATCTCCCTATACGATGCGAGAAATGCTGTTAAAAATGTTGATTTTAAATGATTTA 3111
Db 3121 GCAATGCTCTTATACGATGCGAGAAATGCTGTTAAAAATGTTGATTTTAAATGATTTA 3180
Qy 3112 GCATGCTGGAATGTAAAGGGCATGTAGATGTACAAAGAGGCATCACCGTCTGCTCT 3171
Db 3181 ACATGTTGGAATGTAAAGGGCATGTAGATGTACAAAGAGGCATCATCGTCTCGACCTT 3240
Qy 3172 GTTATCCAGAAATGGAAGAGCAAGAGTGTCACAAGCAGTTTCGCTCTGCTCCGGGGGTGGC 3231
Db 3241 GTTATCCAGAAATGGAAGAGCAAGAGTGTCACAAGCAGTTTCGCTCTGCTCCGGGGGTGGC 3300
Qy 3232 TATATCTCTCGTGTCAAGCGGTACAAAGAGGGATATGAGAGGGTGTGTAAACGATCCAT 3291
Db 3301 TATATCTCTCGTGTCAAGCGGTACAAAGAGGGATATGAGAGGGTGTGTAAACGATCCAT 3360
Qy 3292 GAATTCGAGAACTATACAGCAAACTAAATTTTAAATCTGTGAAGAGAGGAAGTGTAT 3351
Db 3361 GAATTCGAGAACTATACAGCAAACTAAATTTTAAATCTGTGAAGAGAGGAAGTGTAT 3420
Qy 3352 CCAACGGATACAGAAACGTTGATTAATGATTTACTGCACCAAGGTACAGCAGTATGTAAT 3411
Db 3421 CCACGGATACAGAAACGTTGATTAATGATTTACTGCACCAAGGTACAGCAGTATGTAAT 3480
Qy 3412 TCCGTTAATGCTGGATATGAGGATGCAATGAAAGTTGATCTACAGCATCTGTTAATTAC 3471
Db 3481 TCCGTTAATGCTGGATATGAGGATGCAATGAAAGTTGATCTACAGCATCTGTTAATTAC 3540
Qy 3472 AAAACGGATTTAGAAAGAAACGTTATACAGATGTACGAAGAGATAATCATTTGCAATAT 3531
Db 3541 AAAACGGATTTAGAAAGAAACGTTATACAGATGTACGAAGAGATAATCATTTGCAATAT 3600
Qy 3532 GACAGAGGTATGTAATTTATCCACTACCGCTGGTATATGACAAAAGAAATTTAGAA 3591
Db 3601 GACAGAGGTATGTAATTTATCCAGTACCGCTGGTATGTCACAAAAGAAATTTAGAA 3660
Qy 3592 TACTTCCAGAAACCGATTAAGGTATGAGATTTGAGAAACCGAAAGGGAAGTTTAT 3651
Db 3661 TACTTCCAGAAACCGATTAAGGTATGAGATTTGAGAAACCGAAAGGGAAGTTTAT 3720
Qy 3652 GTAGACAGCTGGAAATTTACTCTTATGGAAGAAATAG 3687
Db 3721 GTAGATAGCTGGAACTACTCTCATGGAAGAAATAG 3756

Search completed: November 21, 2004, 13:33:28
Job time : 1492 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 08:48:00 ; Search time 1565 Seconds
(without alignments)
12367.166 Million cell updates/sec

Title: US-10-614-524-1
Perfect score: 3687
Sequence: 1 ttgacttcaatagaaaa.....tactccttatggaggaatag 3687

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001s:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003s:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3687	100.0	3687	AAH28240	Nucleotid
2	3666.2	99.4	4173	AA502482	B. thurin
3	3266.6	88.6	3684	AAV15222	Bacillus
4	3266.6	88.6	3684	AA89221	Bacillus
5	3260.2	88.4	3684	AA502489	B. thurin
6	3132	84.9	4074	AAQ56804	Bacillus
7	2687.2	72.9	3932	AAQ64112	cryET5 ge
8	2687.2	72.9	3932	AAZ09160	B. thurin
9	2687.2	72.9	3934	AAZ09160	DNA encod
10	2687.2	72.9	3934	AAZ09160	cryET5 ge
11	2687.2	72.9	3934	AAZ09160	DNA encod
12	2684.2	72.8	3687	AAV83927	B. thurin
13	2630.2	71.3	3627	AA504854	Bacillus
14	2544.4	69.0	3663	AA500422	B. thurin
15	2541.2	68.9	3663	AA500421	B. thurin
16	2384.2	64.7	3624	AA504853	Bacillus
17	2004.8	54.4	3651	AA504852	Bacillus
18	1793.4	48.6	3522	AAAT1658	B. t. toxi
19	1791.8	48.6	3522	AAQ06830	Sequence
20	1791.8	48.6	3522	AA49592	Bacillus
21	1790.2	48.6	3522	AAQ26928	DNA encod

22	1662	45.1	4106	2	AAV16214	DNA encod
23	1662	45.1	4106	2	AAV09318	Bacillus
24	1581.6	42.9	3558	2	AAZ60619	Polynucle
25	1501	40.7	3766	2	AAQ77858	Crystal p
26	1438.6	39.0	8854	2	AAZ20086	DNA encod
27	1432.4	38.9	3713	2	AAQ64111	cryET4 ge
28	1432.4	38.9	3713	2	AAZ09159	DNA encod
29	1432.4	38.9	3713	2	AAZ09159	DNA encod
30	1432.4	38.9	3713	2	AAZ09159	DNA encod
31	1432.4	38.9	3713	2	AAZ09159	DNA encod
32	1411.4	38.3	4020	2	AAQ14648	cryIF gen
33	1408.4	38.2	3522	2	AAQ10182	Lepidopte
34	1408.4	38.2	3522	2	AAQ47291	Delta end
35	1408.4	38.2	3522	2	AAV62081	Plasmid p
36	1408.4	38.2	3522	2	AAZ60606	Wild-type
37	1408.4	38.2	3522	2	AAZ00565	B. thurin
38	1406.8	38.2	3522	2	AAZ18722	Codon-rew
39	1405.2	38.1	3522	2	AAZ05270	cryIF tox
40	1402.2	38.0	5170	12	ADK98488	B thuring
41	1402.2	38.0	5600	12	ADK98490	B thuring
42	1402.2	38.0	6600	12	ADK98482	B thuring
43	1402.2	38.0	7000	12	ADK98485	B thuring
44	1402	38.0	3534	2	AAV31162	Bacillus
45	1402	38.0	3534	6	ABK11833	DNA encod

ALIGNMENTS

RESULT 1
AAH28240
ID AAH28240 standard; DNA; 3687 BP.
XX
AC AAH28240;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a Cry1Bf insecticidal protein.
XX
KW Cry1Bf; insecticidal protein; Cry1Jd; Cry9Pa; lepidoptera; coleoptera;
insect pest; transgenic plant; ss.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
CDS 1..3687
FT /*tag= a
FT /product= "Cry1Bf insecticidal protein"
XX
FN WO200147952-A2.
XX
PD 05-JUL-2001.
XX
PF 19-DEC-2000; 2000WO-EP013184.
XX
PR 28-DEC-1999; 99US-0173387P.
XX
PA (AVET) AVENTIS CROPS SCIENCE NV.
XX
PI Arnaut G, Beets A, Damme N, Mathieu E, Vanneste S, Van Rie J;
WPI; 2001-425619/45.
DR P-PSDB; AAB84628.
XX
PT Novel insecticidal proteins Cry1Jd, Cry9Pa and Cry1Bf, derived from
Bacillus thuringiensis, useful for controlling insects in plants.
XX
PS Claim 5; Page 30-36; 65pp; English.
XX
CC The present sequence encodes Cry1Bf, an insecticidal protein derived from
Bacillus thuringiensis. The specification also describes Cry1Jd and
Cry9Pa. The Cry proteins have activity against lepidopteran and
coleopteran insect pests. Cry1Bf, Cry1Jd and Cry9Pa polynucleotides and

CC polypeptides are useful for obtaining a plant with resistance to insects.
CC Cry polynucleotides are useful for producing transgenic plants which are
CC resistant to insects

XX	SQ	Sequence	3687 BP; 1219 A; 640 C; 805 G; 1023 T; 0 U; 0 Other;	
		Query Match	100.0%; Score 3687; DB 4; Length 3687;	
		Best Local Similarity	100.0%; Pred. No. 0;	
		Matches 3687; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	TTGACCTTCAAAATAGGAAAAATGAGAAATGAAATTAATAATGCTTTATCGAATTCAGCTGTA	60	
DB	1	TTGACCTTCAAAATAGGAAAAATGAGAAATGAAATTAATAATGCTTTATCGAATTCAGCTGTA	60	
QY	61	TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATTGAGGAAATCTTTGTGT	120	
DB	61	TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATTGAGGAAATCTTTGTGT	120	
QY	121	ATAGCCGAGGGGAATATATCAATCCACTTGTGTTAGCGCATCAACAGTCCAAACGGGTATT	180	
DB	121	ATAGCCGAGGGGAATATATCAATCCACTTGTGTTAGCGCATCAACAGTCCAAACGGGTATT	180	
QY	181	AACATAGCTGGTGAATPACTAGTGTATTAGGGGTACCGTTTGTCTGGACAAATAGCTAGT	240	
DB	181	AACATAGCTGGTGAATPACTAGTGTATTAGGGGTACCGTTTGTCTGGACAAATAGCTAGT	240	
QY	241	TTTTATAGTTTTCTTGTGTGGTGAATTTATGGCCCGCGCGGAGAGATCAGTGGGAAATTTTC	300	
DB	241	TTTTATAGTTTTCTTGTGTGGTGAATTTATGGCCCGCGCGGAGAGATCAGTGGGAAATTTTC	300	
QY	301	CTAGAACATGTCGAACAACTTATAAATCAACAAATAACGAAATGCTAGGAATACGGCA	360	
DB	301	CTAGAACATGTCGAACAACTTATAAATCAACAAATAACGAAATGCTAGGAATACGGCA	360	
QY	361	CTTGCTCGAATPACAAGTTTGGAGATTCCTTTAGAGCTTATCAACAGTCACTTGAAGAT	420	
DB	361	CTTGCTCGAATPACAAGTTTGGAGATTCCTTTAGAGCTTATCAACAGTCACTTGAAGAT	420	
QY	421	TGGCTAGAAACCGTGATGATGATCAAGACGAGAGTGTCTTTATACCCATATATAGCC	480	
DB	421	TGGCTAGAAACCGTGATGATGATCAAGACGAGAGTGTCTTTATACCCATATATAGCC	480	
QY	481	TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAAACCAAGAGTTCCA	540	
DB	481	TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAAACCAAGAGTTCCA	540	
QY	541	TTATTAAATGATATGCTCAAGCTGCAAAATTTACACTATATATATGAGAGATGCTCT	600	
DB	541	TTATTAAATGATATGCTCAAGCTGCAAAATTTACACTATATATATGAGAGATGCTCT	600	
QY	601	CTTTTTGGTGTGAATTTGGGCTTACATCGCAGGAAATCAACGTTTATTATGAGCGCCAA	660	
DB	601	CTTTTTGGTGTGAATTTGGGCTTACATCGCAGGAAATCAACGTTTATTATGAGCGCCAA	660	
QY	661	GTGGAACAAACGAGAGATTATCCGACTATTGCGTAGAATGGTATTAATACAGGTCTAAAT	720	
DB	661	GTGGAACAAACGAGAGATTATCCGACTATTGCGTAGAATGGTATTAATACAGGTCTAAAT	720	
QY	721	AGCTTGAGAGGGAACAAATGCCGAAAGTTGGGTGCGTTAATCAANTCCGTAGAGATCTA	780	
DB	721	AGCTTGAGAGGGAACAAATGCCGAAAGTTGGGTGCGTTAATCAANTCCGTAGAGATCTA	780	
QY	781	ACGTTTAGGGGTATTAGATCTAGTGGCATTATCCCAAGCTATGACACTCGCACTTATCCA	840	
DB	781	ACGTTTAGGGGTATTAGATCTAGTGGCATTATCCCAAGCTATGACACTCGCACTTATCCA	840	
QY	841	ATAAATACGAGTCTCAGTTTAAACAGGGAAGTTTATACAGACCAATTTGGAGCAACAGG	900	
DB	841	ATAAATACGAGTCTCAGTTTAAACAGGGAAGTTTATACAGACCAATTTGGAGCAACAGG	900	
QY	901	GTAATAATGCGAATGATGAATGGTATTAATAAATGCAACCTTCGTTTCCGCTATAGAG	960	
DB	901	GTAATAATGCGAATGATGAATGGTATTAATAAATGCAACCTTCGTTTCCGCTATAGAG	960	

QY	961	ACTGCGGTTATCCGAAGCCCGCATCTACTAGGCAATATGACTTACTGATTTTCTAGAACAACTTACAAATTTTAGC	1020	
DB	961	ACTGCGGTTATCCGAAGCCCGCATCTACTAGGCAATATGACTTACTGATTTTCTAGAACAACTTACAAATTTTAGC	1020	
QY	1021	ACTTCAATCAGATGGAGTGTCTACTAGGCAATATGACTTACTGCGGGGGGACACAAATTCAA	1080	
DB	1021	ACTTCAATCAGATGGAGTGTCTACTAGGCAATATGACTTACTGCGGGGGGACACAAATTCAA	1080	
QY	1081	TCTCGGCCAATAGGAGCGGATTAATACCTCAACGCATGGGTCTACCAATCTCTCTATT	1140	
DB	1081	TCTCGGCCAATAGGAGCGGATTAATACCTCAACGCATGGGTCTACCAATCTCTCTATT	1140	
QY	1141	AATCCTGTAAAGATTATCATTTCTCTCGAGAGCTATATGGACTGAATCATATGACGA	1200	
DB	1141	AATCCTGTAAAGATTATCATTTCTCTCGAGAGCTATATGGACTGAATCATATGACGA	1200	
QY	1201	GTGCTTCTATGGGAATTTACCTTGAACCTTATTCATGGTGTCCCTACTCTGTAGATTAAAT	1260	
DB	1201	GTGCTTCTATGGGAATTTACCTTGAACCTTATTCATGGTGTCCCTACTCTGTAGATTAAAT	1260	
QY	1261	TTTAGGAACCTCAGAAATCTTTTGAAGAGGTACTGTAACTPATATAGTCAACCTATGAG	1320	
DB	1261	TTTAGGAACCTCAGAAATCTTTTGAAGAGGTACTGTAACTPATATAGTCAACCTATGAG	1320	
QY	1321	TCACCTGGGCTTCAATTTAAAGATTTCAGAACTGAAATTTACCACCAAGAAACACAGAACGA	1380	
DB	1321	TCACCTGGGCTTCAATTTAAAGATTTCAGAACTGAAATTTACCACCAAGAAACACAGAACGA	1380	
QY	1381	CCAAATTTAGAAATCATATAGTCTCATAGGTTATCTCATAGGGCTCAATTTCACAATCTAGG	1440	
DB	1381	CCAAATTTAGAAATCATATAGTCTCATAGGTTATCTCATAGGGCTCAATTTCACAATCTAGG	1440	
QY	1441	GTGCATGTACAGTATATTTCTTGGAGCGCACCGTAGTGCAGATCGTACAAATACCATTAGT	1500	
DB	1441	GTGCATGTACAGTATATTTCTTGGAGCGCACCGTAGTGCAGATCGTACAAATACCATTAGT	1500	
QY	1501	TCAGATAGCATTAACACAAATACCATTTGTAATAATCAATTCAACTTAATTCAGGTACTCT	1560	
DB	1501	TCAGATAGCATTAACACAAATACCATTTGTAATAATCAATTCAACTTAATTCAGGTACTCT	1560	
QY	1561	GTAGTCAGTGGCCAGGATTTTACAGGAGGGGATATAATCCGAACTAACCTTAAATGGTAGT	1620	
DB	1561	GTAGTCAGTGGCCAGGATTTTACAGGAGGGGATATAATCCGAACTAACCTTAAATGGTAGT	1620	
QY	1621	GTACTAAGTATGGGTCTTAATTTTAAATAATACATCATTTACAGCGGTATCGCGTAGAGTT	1680	
DB	1621	GTACTAAGTATGGGTCTTAATTTTAAATAATACATCATTTACAGCGGTATCGCGTAGAGTT	1680	
QY	1681	CGTTATGCTGCTTCTCAAAACAATGGTCTGAGGTAACTGTGCGAGGGAGTACTACTTTT	1740	
DB	1681	CGTTATGCTGCTTCTCAAAACAATGGTCTGAGGTAACTGTGCGAGGGAGTACTACTTTT	1740	
QY	1741	GATCAAGGATTCCTTAGTACTATGAGTGCAATAGTCTTTGACATCTCAATCATTTAGA	1800	
DB	1741	GATCAAGGATTCCTTAGTACTATGAGTGCAATAGTCTTTGACATCTCAATCATTTAGA	1800	
QY	1801	TTTGCAGAAATTTCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA	1860	
DB	1801	TTTGCAGAAATTTCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATAAGTATA	1860	
QY	1861	AGTAAATATGCAAGGTAGACAAAAGTTTCACTTTGATATAAATTTCAATTTCCAAATTACT	1920	
DB	1861	AGTAAATATGCAAGGTAGACAAAAGTTTCACTTTGATATAAATTTCAATTTCCAAATTACT	1920	
QY	1921	GCAACCTTCGAAGCAGAAATCGAATTTAGAAAGGGCGCAAGAGCGGTGAATGCTCTGTTT	1980	
DB	1921	GCAACCTTCGAAGCAGAAATCGAATTTAGAAAGGGCGCAAGAGCGGTGAATGCTCTGTTT	1980	
QY	1981	ACTTAATACCAATCCCAAGAGATTTGAAAACAGATGTGACAGATTATCATATTGATCAAGTA	2040	
DB	1981	ACTTAATACCAATCCCAAGAGATTTGAAAACAGATGTGACAGATTATCATATTGATCAAGTA	2040	

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QY 2041 TCCAAATTTAGTCGCGTGTATTCGATGAAATTCCTGTTAGATGAAAAAGAGAGAATTAATCTT 2100
DB 2041 TCCAAATTTAGTCGCGTGTATTCGATGAAATTCCTGTTAGATGAAAAAGAGAGAATTAATCTT 2100
QY 2101 GAGAAAGTCAAAATATGCGAAACGACTCAGTGATGAAAGAACTTACTCCAAGATCCAAC 2160
DB 2101 GAGAAAGTCAAAATATGCGAAACGACTCAGTGATGAAAGAACTTACTCCAAGATCCAAC 2160
QY 2161 TTCAATCCATCAATTAAGCAACACAGACTTCATATCTACTTAATGAGCAATCGAATTTTACA 2220
DB 2161 TTCAATCCATCAATTAAGCAACACAGACTTCATATCTACTTAATGAGCAATCGAATTTTACA 2220
QY 2221 TCTATCCATGAAATCTGAAACATGATGATGCGGGAAGTGAGAACATTAATCAATCCAGGAA 2280
DB 2221 TCTATCCATGAAATCTGAAACATGATGATGCGGGAAGTGAGAACATTAATCAATCCAGGAA 2280
QY 2281 GGAATGACGTAATTTAAGAGAAATTAACGTCACACTACCGGGGACCTTTAATGAGTGTTAT 2340
DB 2281 GGAATGACGTAATTTAAGAGAAATTAACGTCACACTACCGGGGACCTTTAATGAGTGTTAT 2340
QY 2341 CCGACGTAATTTATCAAAAAATAGAGAGTCGGAATTAAGAGCTTATACCTCGCTACCAA 2400
DB 2341 CCGACGTAATTTATCAAAAAATAGAGAGTCGGAATTAAGAGCTTATACCTCGCTACCAA 2400
QY 2401 TTAAGAGGATATTAATGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTTAAATGCG 2460
DB 2401 TTAAGAGGATATTAATGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTTAAATGCG 2460
QY 2461 AAACATGAAACATTTGATGATTCAGGTACCGATCCGATCCGATGCGCGCTTCAGTTGAAAGC 2520
DB 2461 AAACATGAAACATTTGATGATTCAGGTACCGATCCGATCCGATGCGCGCTTCAGTTGAAAGC 2520
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DB 2521 CCAATCGGAAGTTCGGAAGACCGAATCGATCGGACCAATTTTGAATGGAATCCGAT 2580
QY 2581 CTAGATTTCTTCGAGAGATGGAAGAAATGTCGCATCAATCCCATCAATTTCTCTTTG 2640
DB 2581 CTAGATTTCTTCGAGAGATGGAAGAAATGTCGCATCAATCCCATCAATTTCTCTTTG 2640
QY 2641 GATATTTGATTTGGATGACAGACTTGCATGAGATCTAGGCGTGTGGTGTATTCAG 2700
DB 2641 GATATTTGATTTGGATGACAGACTTGCATGAGATCTAGGCGTGTGGTGTATTCAG 2700
QY 2701 ATTAAGACGAGAAAGTTCATCAAGACTAGGGAATCTGGAATTTATTAAGAGAAACA 2760
DB 2701 ATTAAGACGAGAAAGTTCATCAAGACTAGGGAATCTGGAATTTATTAAGAGAAACA 2760
QY 2761 TTATTAGGAGAGCACTGTCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
DB 2761 TTATTAGGAGAGCACTGTCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
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DB 2821 GAAAACTCAATTTGAAACAAACAGATATATACAGAGGCAAAAGAGAGCTGTGATGCT 2880
QY 2881 TTATTGATGATTTCAATATATAGATTTACAGCGGATACAAACATTTGGCATGATTCAT 2940
DB 2881 TTATTGATGATTTCAATATATAGATTTACAGCGGATACAAACATTTGGCATGATTCAT 2940
QY 2941 CGCGCAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTCAGAAATTTCTGTTATC 3000
DB 2941 CGCGCAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTCAGAAATTTCTGTTATC 3000
QY 3001 CGCGGTGTAATTCGGAATTTTGAAGATTTAGAAAGTTCGCAATTTATCACTGCAATCTCC 3060
DB 3001 CGCGGTGTAATTCGGAATTTTGAAGATTTAGAAAGTTCGCAATTTATCACTGCAATCTCC 3060
QY 3061 CTATACGATCGGAGAAATCTGTTTAAATGTTGATTTTAAATGGAATTTAGCATGCTGG 3120
DB 3061 CTATACGATCGGAGAAATCTGTTTAAATGTTGATTTTAAATGGAATTTAGCATGCTGG 3120
QY 3121 AATGTAAGAGGCGATAGATGTACACAGAGCCATCCCGTTCCTGTTCTGTTATCCCA 3180
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DB 3121 AATGTAAGAGGCGATAGATGTACACAGAGCCATCCCGTTCCTGTTCTGTTATCCCA 3180
QY 3181 GAATGGGAGCAGAAAGTGTCAACAGCAGTTCCGCTCTGTCGGGGCGTGGCTATATCTC 3240
DB 3181 GAATGGGAGCAGAAAGTGTCAACAGCAGTTCCGCTCTGTCGGGGCGTGGCTATATCTC 3240
QY 3241 CGTGTCAGCGGTACAAAGAGGATATGAGAGGGTGTGTAAACGATCCATGAAATCGAG 3300
DB 3241 CGTGTCAGCGGTACAAAGAGGATATGAGAGGGTGTGTAAACGATCCATGAAATCGAG 3300
QY 3301 AACAAATACAGACGAACTAAAAATTTAAAACTGTGAAGAGAGAAAGTGTATCCAAACGAT 3360
DB 3301 AACAAATACAGACGAACTAAAAATTTAAAACTGTGAAGAGAGAAAGTGTATCCAAACGAT 3360
QY 3361 ACAGGACGCTGAATGATTTACTGCACCAAGGTACAGCAGTATGTAATTTCCGTAAT 3420
DB 3361 ACAGGACGCTGAATGATTTACTGCACCAAGGTACAGCAGTATGTAATTTCCGTAAT 3420
QY 3421 GCTGATATGAGGATGCATATGAACTGATACAGCATCTGTTAAATTTACAAACCGACT 3480
DB 3421 GCTGATATGAGGATGCATATGAACTGATACAGCATCTGTTAAATTTACAAACCGACT 3480
QY 3481 TATGAAGAGAAACGATATACAGATGTACGAAGAGATAATCATTTGTAATATGACAGAGGG 3540
DB 3481 TATGAAGAGAAACGATATACAGATGTACGAAGAGATAATCATTTGTAATATGACAGAGGG 3540
QY 3541 TATGTAATTTACCACTACCACTACCACTGTTATATGACAAAAGATTTAGAAATCTCCCA 3600
DB 3541 TATGTAATTTACCACTACCACTACCACTGTTATATGACAAAAGATTTAGAAATCTCCCA 3600
QY 3601 GAAACCGAATAAGGTATGATTTGAGATTGGAGAAACGGAAGGAGAGTATTATTGTAGACAGC 3660
DB 3601 GAAACCGAATAAGGTATGATTTGAGATTGGAGAAACGGAAGGAGAGTATTATTGTAGACAGC 3660
QY 3661 GTGGAATTTACTCTTTATGAGAGAAATAG 3687
DB 3661 GTGGAATTTACTCTTTATGAGAGAAATAG 3687

RESULT 2
AAS02482
ID AAS02482 standard; DNA; 4173 BP.
XX
AC AAS02482;
XX
DT 29-AUG-2001 (first entry)
XX
DE
DE B. thuringiensis DNA encoding a toxic crystal protein, CryET64.
KW Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; yre; sorghum;
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
KW cotton leaf perforator; CryET64; ds.
XX
OS Bacillus thuringiensis.
XX
Key Location/Qualifiers
CDS 1..3471
FT /*tag= a
FT /product= "CryET64"
FT /trans_except= (pos:1..3,aa:Met)
XX
WO200119859-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US025361.
XX
PR 15-SEP-1999; 99US-0153995P.
XX
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(MONS) MONSANTO CO.

PA Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
 XX WPI; 2001-281518/29.
 XX P-PSDB; AAU02039.

Lepidopteran-active *Bacillus thuringiensis* delta-endotoxin polypeptides
 PT and the polynucleotides that encode them, useful for increasing the
 XX insect resistance of plant.

XX Claim 17; Page 133-138; 173pp; English.

XX The sequence encodes a *B. thuringiensis* Lepidopteran-active delta-
 CC endotoxin, crystal protein CryIb4. The Lepidopteran-active *B.*
 CC *thuringiensis* delta-endotoxin polypeptides may be used as compositions
 CC that are applied to plant crops to protect them from insect damage. The
 CC polynucleotides may be used in the production of transgenic plants that
 CC express the insecticidal polypeptides and consequently have improved
 CC insect resistance compared to non-transformed plants. Monocotyledonous or
 CC dicotyledonous plants may be protected in this way, for example corn,
 CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 CC cotton leaf perforator and spruce budworm) may be affected by application
 CC of the insecticidal polypeptides (full details given in specification)

XX Sequence 4173 BP; 1417 A; 705 C; 878 G; 1173 T; 0 U; 0 Other;

Query Match 99.4%; Score 3666.2; DB 4; Length 4173;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 3674; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TTGACTTCAAAATAGGAAAAATGAGAAATGAAATTAATAATCTTTATCGATTCACGCTGTA 60
 Db 1 TTGACTTCAAAATAGGAAAAATGAGAAATGAAATTAATAATCTTTATCGATTCACGCTGTA 60

Qy 61 TCGAATCATTTCCACAAATGGATCTATACCAAGATGCTCGTATTCAGGATCTTTGTGT 120
 Db 61 TCGAATCATTTCCACAAATGGATCTATACCAAGATGCTCGTATTCAGGATCTTTGTGT 120

Qy 121 ATAGCCGAGGGGAATTAATCAATCCACTTGTAGGCGATCAACAGTCCAAAGCGGTATT 180
 Db 121 ATAGCCGAGGGGAATTAATCAATCCACTTGTAGGCGATCAACAGTCCAAAGCGGTATT 180

Qy 181 AACATAGCTGGTAGAATACATAGGTGTATTTAGGCGTACCGTTTCTGGACAAATAGTAGT 240
 Db 181 AACATAGCTGGTAGAATACATAGGTGTATTTAGGCGTACCGTTTCTGGACAAATAGTAGT 240

Qy 241 TTTTATATGTTTCTTGTGTGTAATATATGCCCCCGGCGAGAGATCAGTGGGAAATTTTC 300
 Db 241 TTTTATATGTTTCTTGTGTGTAATATATGCCCCCGGCGAGAGATCAGTGGGAAATTTTC 300

Qy 301 CTAGAACATGCGAACAACTTATAATCAACAAATACAGAAATGCTAGGAATACGGCA 360
 Db 301 CTAGAACATGCGAACAACTTATAATCAACAAATACAGAAATGCTAGGAATACGGCA 360

Qy 361 CTTGCTCGATTACAGGTTTAGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
 Db 361 CTTGCTCGATTACAGGTTTAGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420

Qy 421 TGGCTAGAAAACCGTGATGATCAAGAACGAGAAGTGTTCTTTATACCCAAATATATAGCC 480
 Db 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTTCTTTATACCCAAATATATAGCC 480

Qy 481 TTAGAACTTGAATTTCTTAATGCGATGCCGTTTTCGCAATTAGAAACCAAGAAGTTCCA 540
 Db 481 TTAGAACTTGAATTTCTTAATGCGATGCCGTTTTCGCAATTAGAAACCAAGAAGTTCCA 540

Qy 541 TTATTAATGCTATGCTCAAGCTGCAAAATTTACCTTATTTATTTAGAGATGCTCT 600
 Db 541 TTATTAATGCTATGCTCAAGCTGCAAAATTTACCTTATTTATTTAGAGATGCTCT 600

Qy 601 CTTTGTGTAGTAGAATTTGGGCTTACATCGCAGGAAATCAACGTTATTATGAGCGCAA 660
 Db 601 CTTTGTGTAGTAGAATTTGGGCTTACATCGCAGGAAATCAACGTTATTATGAGCGCAA 660

Qy 661 GTGGAAACAAACGAGAGATTATTTCCGACTATTTGGGTAGAAATGGTATTAATACAGGCTTAAAT 720
 Db 661 GTGGAAACAAACGAGAGATTATTTCCGACTATTTGGGTAGAAATGGTATTAATACAGGCTTAAAT 720

Qy 721 AGCTTCAGAGAGGACAAATGCCCAAGTGGGTGCGTTATAATCAATTCGCTAGAGATCTA 780
 Db 721 AGCTTCAGAGAGGACAAATGCCCAAGTGGGTGCGTTATAATCAATTCGCTAGAGATCTA 780

Qy 781 ACCTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
 Db 781 ACCTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840

Qy 841 ATAAATACAGTGCCTCAGTTAAACAGGGAAGTTTATACAGAGCAATTTGGAGCAACAGGG 900
 Db 841 ATAAATACAGTGCCTCAGTTAAACAGGGAAGTTTATACAGAGCAATTTGGAGCAACAGGG 900

Qy 901 GTAAATATGCGCAAGTATGAAATGGTATAATAATGCAACCTTCGTTTCCGCTATAGAG 960
 Db 901 GTAAATATGCGCAAGTATGAAATGGTATAATAATGCAACCTTCGTTTCCGCTATAGAG 960

Qy 961 ACTGGGGTATCCGAAGCCCGCATCTACTGATTTTCTAGAACAACTTACAAATTTTAGC 1020
 Db 961 ACTGGGGTATCCGAAGCCCGCATCTACTGATTTTCTAGAACAACTTACAAATTTTAGC 1020

Qy 1021 ACTTCATACAGATGAGTGTACTACTAGGCATATAGCTTACTGGGGGGGACACAAATTTCAA 1080
 Db 1021 ACTTCATACAGATGAGTGTACTACTAGGCATATAGCTTACTGGGGGGGACACAAATTTCAA 1080

Qy 1081 TCTCGGCCAATAGGAGGGGATTAATATACCTCAACGCGATGGTCTACCAATATCTTCTATT 1140
 Db 1081 TCTCGGCCAATAGGAGGGGATTAATATACCTCAACGCGATGGTCTACCAATATCTTCTATT 1140

Qy 1141 AATCTGTAGAGATTCATCTCTCTCGAGAGGTATTTGGAGCTGAATCATATGCGAGA 1200
 Db 1141 AATCTGTAGAGATTCATCTCTCTCGAGAGGTATTTGGAGCTGAATCATATGCGAGA 1200

Qy 1201 GTGCTTCTATGGGAAATTTACCTTGAACCTATTCATGGTGTCCCTACTCTAGATTTAAT 1260
 Db 1201 GTGCTTCTATGGGAAATTTACCTTGAACCTATTCATGGTGTCCCTACTCTAGATTTAAT 1260

Qy 1261 TTTAGGAACCTTCAGAAATCTTTTGAAGAGTACTGTCTAATAGTCAACCCCTATGAG 1320
 Db 1261 TTTAGGAACCTTCAGAAATCTTTTGAAGAGTACTGTCTAATAGTCAACCCCTATGAG 1320

Qy 1321 TCACCTGGGCTTCAATTAAGATTTCAAGAACTGAATTAACACCAAGAAACAAAGAACGA 1380
 Db 1321 TCACCTGGGCTTCAATTAAGATTTCAAGAACTGAATTAACACCAAGAAACAAAGAACGA 1380

Qy 1381 CCAAAATATGAATCATATAGTCAATAGTGTATCTCAATAGGGCTCATTTTCAAAATCTAG 1440
 Db 1381 CCAAAATATGAATCATATAGTCAATAGTGTATCTCAATAGGGCTCATTTTCAAAATCTAG 1440

Qy 1441 GTGCAATGATACAGTATATTTCTTGGAGCGCACCGGTATGCGAGATCGTACAAATACCTTAGT 1500
 Db 1441 GTGCAATGATACAGTATATTTCTTGGAGCGCACCGGTATGCGAGATCGTACAAATACCTTAGT 1500

Qy 1501 TCAGATAGCATAAACAAATACCATTTGGTAAATCATTTCAACCTTAAATTCAGGTACCTCT 1560
 Db 1501 TCAGATAGCATAAACAAATACCATTTGGTAAATCATTTCAACCTTAAATTCAGGTACCTCT 1560

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Qy 1621 GTACTAAGTATGGGCTTAAATTTTAAATATACATCATTTACAGCGGTATCGCGTAGAGTT 1680
 Db 1621 GTACTAAGTATGGGCTTAAATTTTAAATATACATCATTTACAGCGGTATCGCGTAGAGTT 1680

1681 CGTTATGCTGCTCTCAAAACAATGCTGCTGAGGGTAACCTGTCGGAGGAGTACTACTTTT 1740
1681 CGTTATGCTGCTCTCAAAACAATGCTGCTGAGGGTAACCTGTCGGAGGAGTACTACTTTT 1740
1741 GATCAAGGATCCCTAGTACTATGATGCAAAATGAGTCTTTTGACATCTCAATCATTTAGA 1800
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1861 AGTAATATGAGGATGAGCAAAAGCTTTCACTTTGTATAAAATGAAATCAATTCCAATTA 1920
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1981 ACTAATACGAATCCAAAGAGATTGAAAACAGATGTGACAGATTATCATATTGATCAAGTA 2040
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2221 TCTATCCATGAACTCTGAAATGAGTGGGAGTGGGAGTGAACATTTACATCCAGAA 2280
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2461 AAACATGAAACATTTGGATGTTCCAGTACCGATCCGATCCGATCCGCTTTCAAGTGAAGC 2520
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2641 GATATTGATTTGGATGACAGACTTGCATGAGATCTAGCGGTGGGTGATTTCAAG 2700
2641 GATATTGATTTGGATGACAGACTTGCATGAGATCTAGCGGTGGGTGATTTCAAG 2700
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2701 ATTAAGCGCAGGAAGTCTAGCAAGACTTAGGGAATCTGGAAATTTATTTGAAGAGAAACCA 2760
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2821 GAAAACTACCAATTTGGAAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTGATGCT 2880
2881 TTATTGTAGATTTCTCAATATAATAGATTACAGCGGATACAAACATTTGGCATGATTCAT 2940
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2941 GCGGAGATAAACTTTGTTTCATCGAATTCGAGAGGCTTATCTGTCAAGAAATATCTGTTATC 3000
3001 CCGGCTGTAATCGGAAATTTTGAAGAAATTTAGAGGTCGCAATTCATCTGCAATCTCC 3060
3001 CCGGCTGTAATCGGAAATTTTGAAGAAATTTAGAGGTCGCAATTCATCTGCAATCTCC 3060
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3181 GAATGGGAGCAGAGTGTCAACAGAGCTTCCGCTCTGTCGGGGCGGTATATCTC 3240
3181 GAATGGGAGCAGAGTGTCAACAGAGCTTCCGCTCTGTCGGGGCGGTATATCTC 3240
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3601 GAAACCGATAGGTTATGAGATTGAGATTGGAGAAACGGAAGGAAATTTATTTGAGACAGC 3660
3601 GAAACCGATAGGTTATGAGATTGAGATTGGAGAAACGGAAGGAAATTTATTTGAGACAGC 3660
3661 GTGAAATTTCTCTTTATGGAGGAATAG 3687
3661 ATAGAATTTCTCTTTATGGAGGAATAG 3687

RESULT 3

AAV15222
ID AAV15222 standard; DNA; 3684 BP.

XX AC AAV15222;

XX DT 27-MAY-1998 (first entry)

XX DE Bacillus thuringiensis 158C2c toxin encoding DNA.

Db 1372 GAAAGCCAAATTAATGAATCTTACAGTCAATAGATTATCTAAATATAAGACTAATATCAAGA 1431
Qy 1435 TCTAGGGTCATGTACCAAGTATATCTTGGAGCGCACCGTAGTGCAGATCGTACAAATACC 1494
Db 1432 AACACTTTGAGAGCACCAGTATATCTTGGACGCACCGTAGTGCAGATCGTACAAATACC 1491
Qy 1495 ATTAGTTCAGATAGCANTAAACAAATACATTTGGTAAATATCAATCTTAATTCAGGT 1554
Db 1492 ATTAGTTCAGATAGCANTAAACAAATACATTTGGTAAATATCAATCTTAATTCAGGT 1551
Qy 1555 ACTCTGTAGTCAGTGGCCAGGATTTACAGAGGCGGATATATCCGAACTAAACGTTAAT 1614
Db 1552 ACTCTGTAGTCAGTGGCCAGGATTTACAGAGGCGGATATATCCGAACTAAACGTTAAT 1611
Qy 1615 GGTAGTGTACTAAGTATGGTCTTAAATTTTAAATATACATCAATACAGCGGTATCGCGTG 1674
Db 1612 GGTAGTGTACTAAGTATGGTCTTAAATTTTAAATATACATCAATACAGCGGTATCGCGTG 1671
Qy 1675 AGAGTTCTGTATGCTGCTCTCAAAACAATGGTCTGAGGGTAACTGTGCGAGGAGTACT 1734
Db 1672 AGAGTTCTGTATGCTGCTCTCAAAACAATGGTCTGAGGGTAACTGTGCGAGGAGTACT 1731
Qy 1735 ACTTTTGTATCAAGGATTCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCA 1794
Db 1732 ACTTTTGTATCAAGGATTCCTAGTACTATGAGTGCAAATGAGTCTTTGACATCTCAATCA 1791
Qy 1795 TTTAGATTTGCAAGATTTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854
Db 1792 TTTAGATTTGCAAGATTTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1851
Qy 1855 AGTATAAGTAATAATGCGAGGTAGACAAACGTTTCTACTTTGATPAAAAATGAAATTCATCCA 1914
Db 1852 AGTATAAGTAATAATGCGAGGTAGACAAACGTTTCTACTTTGATPAAAAATGAAATTCATCCA 1911
Qy 1915 ATTACTGCAACCTCGAGAGCAATACGATTTAGAAAGGGCGCAGAGCGGTGATGCT 1974
Db 1912 ATTACTGCAACCTCGAGAGCAATATGATTTAGAAAGGGCGCAGAGCGGTGATGCT 1971
Qy 1975 CTGTTTACTAATACGAATCCAAAGAGATTTGAAACAGATGTGACAGATTTATCATATTGAT 2034
Db 1972 CTGTTTACTAATACGAATCCAAAGAGGTGTAACACAGGTGTGACAGATTTATCATATTGAT 2031
Qy 2035 CAAATATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGCTTAGATGAAAGAGAGAA 2094
Db 2032 CAAATATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGCTTAGATGAAAGAGAGAA 2091
Qy 2095 TTACTTGAGAAAGTGAATATCGGAAACGACTCAGTGTATGAAAGAACTTACTCCAGAT 2154
Db 2092 TTACTTGAGAAAGTGAATATCGGAAACGACTCAGTGTATGAAAGAACTTACTCCAGAT 2151
Qy 2155 CCAAACTTCAATCCATCAATGAAGCAACAGACTTCTATCTATCTAATGAGCAATCGAAT 2214
Db 2152 CCAAACTTCAATCCATCAATGAAGCAACAGACTTCTATCTATCTAATGAGCAATCGAAT 2211
Qy 2215 TTCAATCTATCCATGAACAAATCTGAAACATGATGGTGGGAGGTGAGAACATTAACAATC 2274
Db 2212 TTCAATCTATCCATGAACAAATCTGAAACATGATGGTGGGAGGTGAGAACATTAACAATC 2271
Qy 2275 CAGGAGGAAATGAGTATTTAAGAGAAATACGTCACACTACCGGGAGCTTTTAAATGAG 2334
Db 2272 CAGGAGGAAATGAGTATTTAAGAGAAATACGTCACACTACCGGGAGCTTTTAAATGAG 2331
Qy 2335 TGTATTCGAGCGTATTTATCAAAAAATAGGAGAGTCCGAAATTAAGCTTATACTCGC 2394
Db 2332 TGTATTCGAGCGTATTTATCAAAAAATAGGAGAGTCCGAAATTAAGCTTATACTCGC 2391
Qy 2395 TACCAATTAAGAGGTATATTGAAGATAGTCAAGATTTTAGAGATATATTGATTCGTTAT 2454
Db 2392 TACCAATTAAGTGGCTATATTGAAGATAGTCAAGATTTTAGAGATATATTGATTCGTTAT 2451
Qy 2455 AATGCGAAACATGAACATTTGATGTTCCAGGTACCGAGTCCGATGCGCGCTTTCAGTT 2514
Db 2452 AATGCGAAACATGAACATTTGATGTTCCAGGTACCGAGTCCGATGCGCGCTTTCAGTT 2511

Qy 2515 GAAAGCCCAATCGGAAGGTGGGAGAACCGAATCGATCGCACCAACATTTTGAATGGAAT 2574
Db 2512 GAAAGCCCAATCGGAAGGTGGGAGAACCGAATCGATCGCACCAACATTTTGAATGGAAT 2571
Qy 2575 CCTGATCTAGATATTGTTCTCTGACAGATGAGAGAAAATGTGCGCATCATTTCCCATCTTTC 2634
Db 2572 CCTGATCTAGATATTGTTCTCTGACAGATGAGAGAAAATGTGCGCATCATTTCCCATCTTTC 2631
Qy 2635 TCTTTGGATATTGATATTGGATGACACAGCTTGCATAGAAATCTAGGCGTGGGTGGTA 2694
Db 2632 TCTTTGGATATTGATATTGGATGACATAGCTTGCATAGAAACCTTAGGCGTGGGTGGTA 2691
Qy 2695 TTCAAGATTAAGACGACAGAAAGGTCAATCAAGACTTAGGGAATCTCGAAATTTATTGAAGAG 2754
Db 2692 TTCAAGATTAAGACGACAGAAAGGTCAATCAAGACTTAGGGAATTTATTGAAGAG 2751
Qy 2755 AAAACATTTATTAGGAGAAAGCACTGTCTCTGTGTGAAGAGAGAGAGAAAATTTGAAGAGAC 2814
Db 2752 AAAACATTTATTAGGAGAAAGCACTGTCTCTGTGTGAAGAGAGAGAGAAAATTTGAAGAGAC 2811
Qy 2815 AAAACGTGAAAACACTACAAATTCGAAACAAAACGAGTATATACAGAGGCAAAAAGAGCTGTG 2874
Db 2812 AAAACGTGAAAACACTACAAATTCGAAACAAAACGAGTATATACAGAGGCAAAAAGAGCTGTG 2871
Qy 2875 GATGCTTTATTGTAGATTCTCAATATATAGATTACAAAGCGGATACAAAACATTTGGCATG 2934
Db 2872 GATGCTTTATTGTAGATTCTCAATATATAGATTACAAAGCGGATACAAAACATTTGGCATG 2931
Qy 2935 ATTCAATGCGGAGATATAAATCTTGTTCATCGAATTTGAGAGGCTTATCTCTCAGAAATTTATCT 2994
Db 2932 ATTCAATGCGGAGATATAAATCTTGTTCATCGAATTTGAGAGGCGTATCTTTTCAGAAATTTATCT 2991
Qy 2995 GTTATCCCGGTGTAAATGCGGAAATTTTTCGAAATTTAGAGGTCGCAATTTACTCTCA 3054
Db 2992 GTTATCCCGGTGTAAATGCGGAAATTTTTCGAAATTTAGAGGTCGCAATTTACTCTCA 3051
Qy 3055 ATCTCCCTATACGATCGGAGAAATGCTCGTTAAAAATGCTGATTTTAAATAGGATTTAGCA 3114
Db 3052 ATCTCCCTATACGATCGGAGAAATGCTCGTTAAAAATGCTGATTTTAAATAGGATTTAGCA 3111
Qy 3115 TGCTGGAATGTAAAGGGCATGTAGTACAAACAGAGCCATCACCGTTCCTCTGTT 3174
Db 3112 TGCTGGAATGTAAAGGGCATGTAGTACAAACAGAGCCATCACCGTTCCTCTGTT 3171
Qy 3175 ATCCAGAAATCGGAGAGAGAGTGTCAACAGCGTTTCGCTGTGTCGCGGGCGTGGCTAT 3234
Db 3172 ATCCAGAAATCGGAGAGAGAGTGTCAACAGCGTTTCGCTGTGTCGCGGGCGTGGCTAT 3231
Qy 3235 ATCTCTCCGTGTACAGCGGTACAAAGAGGATATGGAGAGGTTGTGTAAACGATCCATGAA 3294
Db 3232 ATCTCTCCGTGTACAGCGGTACAAAGAGGATATGGAGAGGTTGTGTAAACGATCCATGAA 3291
Qy 3295 ATCGAGAAACATACAGAGCAACTAAAAATTTAAAACTGTGAAAGAGAGAGTGTATCCA 3354
Db 3292 ATCGAGAAACATACAGAGCAACTAAAAATTTAAAACTGTGAAAGAGAGAGTGTATCCA 3351
Qy 3355 ACAGATACAGGAACTGTAAATGATTTACTGCAACCAAGGTACAGAGTATGTAATTC 3414
Db 3352 ACAGATACAGGAACTGTAAATGATTTACTGCAACCAAGGTACAGAGTATGTAATTC 3411
Qy 3415 CGTAATCTGATATGAGGATGATGAACTGTGATCTACAGCATCTGTTAAATTTACAAA 3474
Db 3412 CGTAATCTGATATGAGGATGATGAACTGTGATCTACAGCATCTGTTAAATTTACAAA 3471
Qy 3475 CCGACTTATGAAGAGAGAAACGATACAGATGTACGAGAGATAATTCATTTGAAATGAC 3534
Db 3472 CCGACTTATGAAGAGAGAAACGATACAGATGTACGAGAGATAATTCATTTGAAATGAC 3531
Qy 3535 AGAGGATGTGAATTTATCCACCACTACCGCTGTTATATGACAAAGAAATTTAGAAATAC 3594
Db 3532 AGAGGATGTGAATTTATCCACCACTACCGCTGTTATATGACAAAGAAATTTAGAAATAC 3591

QY	1195	GCAGGAGTGCCTTCTATGCGGGAATTTACCTTGAACCTTATTCATGCTGTGCCCTACTGTGTAGA	1254
DB	1201	GCAGGGAATAATAT-----ACTTCTAACTACTCTGTGAATGAGTACCTTGGCGCTAGA	1254
QY	1255	TTTAATTTTAGGAACCCCTCAGAACTACTTTTGAAGAGAGTACTGCTAACTACTAGTCAACCC	1314
DB	1255	TTTAAATTGGAGAAATCCCGTGAATTCCTT---AGAGTGACCTTCTCTATACTATATAGG	1311
QY	1315	TATGAGTCACTCGGCGCTTCAAATTAAGAATTCAGAAACTGAATTTACACAGAGAAACAACA	1374
DB	1312	TATACTGGAGTGGGACACAACTATTTGATTTAGAACTGAAATTTACACAGAGAAACAACA	1371
QY	1375	GAAAGCAAAATTAATGAATCATATAGTCAATAGGTATCTCACATAGGGCTCATTTTCAAA	1434
DB	1372	GAAAGCAAAATTAATGAATCTTACAGTCAATAGATTTATCTAATAAAGACTAATATCAGGA	1431
QY	1435	TCTAGGGTGCAATGTACCAAGTATATTTCTTGAGCGCACCGTGTAGTCAGAGATCGTACAAATACC	1494
DB	1432	AACACTTTGAGAGCACCAAGTATATCTTGGACGACCGTGTAGTCAGATCGTACAAATACC	1491
QY	1495	ATTAGTTCAGATAGATAACAACAATACCAATGTGTAAATCATTTCAAACCTTAATTCAGGT	1554
DB	1492	ATTAGTTCAGATAGATAACAACAATACCAATTTGGTAAATCAITTTCAAACCTTAATTCAGGT	1551
QY	1555	ACCTCTGTAGTACGTGGCCAGGATTTACAGGAGGGATATATCCGAACCTAAGCTTAAT	1614
DB	1552	ACCTCTGTAGTACGTGGCCAGGATTTACAGGAGGGATATATCCGAACCTAAGCTTAAT	1611
QY	1615	GGTAGTGTACTAAAGTATGGGTCTTAAATTTTAAATAATACATCAITTTACAGCGGTATCGCGTG	1674
DB	1612	GGTAGTGTACTAAAGTATGGGTCTTAAATTTTAAATAATACATCAITTTACAGCGGTATCGCGTG	1671
QY	1675	AGAGTTGGTTATGCTGCTTCTCAAAACAATGGTCTCTGAGGGTAACTGTCTGAGGAGGAGTACT	1734
DB	1672	AGAGTTGGTTATGCTGCTTCTCAAAACAATGGTCTCTGAGGGTAACTGTCTGAGGAGGAGTACT	1731
QY	1735	ACTTTTGATCAAGGATTTCCCTAGTACTATGAGTGCBAATGAGTCTTTTGACATCTCAATCA	1794
DB	1732	ACTTTTGATCAAGGATTTCCCTAGTACTATGAGTGCBAATGAGTCTTTTGACATCTCAATCA	1791
QY	1795	TTTAGATTTGCAGAAATTTCCCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA	1854
DB	1792	TTTAGATTTGCAGAAATTTCCCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGAATA	1851
QY	1855	AGTATAGTAATAATGCAAGGTAGACAAACGGTTTCACCTTTGATATAAATGAAATTCATTTCCA	1914
DB	1852	AGTATAGTAATAATGCAAGGTAGACAAACGGTTTCACCTTTGATATAAATGAAATTCATTTCCA	1911
QY	1915	ATTACTGCACCTTCGAGCAGAAATACGATTTAGAAAGGCGCAAGGCGGTGGAATGCT	1974
DB	1912	ATTACTGCACCTTCGAGCAGAAATACGATTTAGAAAGGCGCAAGGCGGTGGAATGCT	1971
QY	1975	CTGTGTTACTAATACGAATCCAAGAGAGATTTGAAAAACAGATGTGACAGATTATCATATTGAT	2034
DB	1972	CTGTGTTACTAATACGAATCCAAGAGAGATTTGAAAAACAGATGTGACAGATTATCATATTGAT	2031
QY	2035	CAAGTATCCAAATTTAGTGGCGTGTATTTCGGATGAATTTCTGCTTAGAGTAAAGAGAGAA	2094
DB	2032	GAAGTATCCAAATTTAGTGGCGTGTATTTCGGATGAATTTCTGCTTAGAGTAAAGAGAGAA	2091
QY	2095	TTACTTCGAGAAAGTAAATATGCCAAACGACTCAAGTCAAGAAAGAACTTTACTTCCAGAT	2154
DB	2092	TTACTTCGAGAAAGTAAATATGCCAAACGACTCAAGTCAAGAAAGAACTTTACTTCCAGAT	2151
QY	2155	CCAAACTTTCACATCCATCAATTAAGCAACACGACTTTCATATCTACTAATGAGCAATCGAAT	2214
DB	2152	CCAAACTTTCACATCCATCAATTAAGCAACACGACTTTCATATCTACTAATGAGCAATCGAAT	2211
QY	2215	TTGACATCTATCCATGAAACAACTGTGAACATGGATGGTGGGGAAGTGAGAACTTACACATC	2274
DB	2212	TTGACATCTATCCATGAAACAACTGTGAACATGGATGGTGGGGAAGTGAGAACTTACACATC	2271

QY	2275	CAGGAAGAAATGACGTAATTTATAAAGAAATTCAGTCACTACCGGGACCTTTTAATGAG	2334
DB	2272	CAGGAAGAAATGACGTAATTTAAAGGAAATTCAGTCACTACCGGGTACTTTTAATGAG	2331
QY	2335	TGTTATCCGACGTATTTATACAAAAATAGGAGAGTCGGAAATTAAGAGCTTATACCTCGC	2394
DB	2332	TGTTATCCGACGTATTTATACAAAAATAGGGAGCGGAAATTAAGGCTTATACCTCGC	2391
QY	2395	TACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAT	2454
DB	2392	TACCAATTAAGTGGCTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTAC	2451
QY	2455	AATCGGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCGATGCGCGCTTTCAGTT	2514
DB	2452	AATCGGAAACATGAAACATTTGGATGTTTCCAGGTACCGAGTCGATGCGCGCTTTCAGTT	2511
QY	2515	GAAGCCCAATCGGAAGTCGGAGAACCAATCGATCGGCACCAATTTTGAATGGAAT	2574
DB	2512	GAAGCCCAATCGGAAGTCGGAGAACCGAATCGATCGGCACCAATTTTGAATGGAAT	2571
QY	2575	CCTGATCTAGATTTGTTCTTCGAGAGATGGAGAAAAATGTGCGCATCATTTCCCATCATTTTC	2634
DB	2572	CCTGATCTAGATTTGTTCTTCGAGAGATGGAGAAAAATGTGCGCATCATTTCCCATCATTTTC	2631
QY	2635	TCCTTGATATATGATATTTGATATGACAGACTTCGATGAGAAATCTAGCGGTGCGGTG67TA	2694
DB	2632	TCCTTGATATATGATATTTGATATGATAGACTTCGATGAGAAATCTAGCGGTGCGGTG67TA	2691
QY	2695	TTCAAGATTAAAGCGCAGGAAGTCATGCAAGACTAGGGAATCTCGAATTTATTTGAAGAG	2754
DB	2692	TTCAAGATTAAAGCGCAGGAAGTCATGCAAGACTAGGGAATCTCGAATTTATTTGAAGAG	2751
QY	2755	AAACCATTAATTAGGAAGACACTGTCGTGTGAAAGAGACAGAGAAAAATCGAGAGAC	2814
DB	2752	AAACCATTAATTAGGAAGACACTGTCGTGTGAAAGAGACAGAGAAAAATCGAGAGAC	2811
QY	2815	AAACGTGAAAAACTCAATTTGGAAAAAACAAGAGTATATACAGAGGCAAAAGAGCTGTG	2874
DB	2812	AAACGTGAAAAACTCAATTTGGAAAAAACAAGAGTATATACAGAGGCAAAAGAGCTGTG	2871
QY	2875	GATGCTTTATTTGTAGATTCTCAATATATAGATTACAGCGGATCAACAATTCGCAATG	2934
DB	2872	GATGCTTTATTTGTAGATTCTCAATATATAGATTACAGCGGATCAACAATTCGCAATG	2931
QY	2935	ATTCATCGCGCAGATAAATCTGTTTCATCGAATTCGAGAGCTTATCTGTGAGAAATTTATCT	2994
DB	2932	ATTCATCGCGCAGATAAATCTGTTTCATCGAATTCGAGAGCTTATCTTTCAGAAATTTATCT	2991
QY	2995	GTTATCCCGGTGTAAATCGGAAATTTTGAAGAAATTAAGAGGTCCGATTAATCACTGCA	3054
DB	2992	GTTATCCAGGTGTAAATCGGAAATTTTGAAGAAATTAAGAGGTCCGATTAATCACTGCA	3051
QY	3055	ATCTCCCTATACGATCGGAGAAATGTCGTTAAAAATGGTGATTTTAATTAATGGAATTAGCA	3114
DB	3052	ATCTCCCTATACGATCGGAGAAATGTCGTTAAAAATGGTGATTTTAATTAATGGAATTAGCA	3111
QY	3115	TGCTGGAATGTAAAAAGGCAATGTAGATGTACAACAGAGCCATCACCGTTCGTGCTTGT	3174
DB	3112	TGCTGGAATGTAAAAAGGCAATGTAGATGTACAACAGAGCCATCACCGTTCGTGCTTGT	3171
QY	3175	ATCCAGAAATGGGAAGCAGAAAGTGTCAACAGAGTTTCGCGTGTGTCGCGGGCGTGCTAT	3234
DB	3172	ATCCAGAAATGGGAAGCAGAAAGTGTCAACAGAGTTTCGCGTGTGTCGCGGGCGTGCTAT	3231
QY	3235	ATCCTCCGTGTCAACGGTACAAAGAGGATATGGAGAGGGTTGTGTACGATCCATGAA	3294
DB	3232	ATCCTCCGTGTCAACGGTACAAAGAGGATATGGAGAGGGTTGTGTACGATCCATGAA	3291
QY	3295	ATCGAGAACAAATACAGACGAATCTAAATTTAAAAAATCTGTGAAGAGGAGGTATCCA	3354
DB	3292	ATCGAGAACAAATACAGACGAATCTAAATTTAAAAAATCTGTGAAGAGGAGGTATCCA	3351
QY	3355	ACGGATACAGGAACGTGTATATGATTTACTGCAACCAAGGTTACAGCATGTATGTAATTC	3414

Db 721 AATTGAGAGGAGCAAAATGCTGAAAGTTGGTTGCGATATAAATCAATTCCTGATAGACTTGA 780
Qy 781 AGCTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACATCGCACTTATCCA 840
Db 781 ACCTAGGAGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACATCGGCTTTATCCA 840
Qy 841 ATAAATACAGAGTCTCAGTTTAAACAGGGAAGTTTATPACAGCGCAATTGGAGCAACAGGG 900
Db 841 ATGAATPACAGTCTCAATTAACAGAGAAATTTATPACAGATCCCAATTTGGGAGAACAAAT 900
Qy 901 GTAAAT-----ATGCGAAGTAAATGGGTATATAATAATGCAACCTTCGTTTCCGCT 954
Db 901 GCACCTTCAGGATTTGCAAGTACGAATGGTTTAAATAATATGCAACCATCGTTTCTGCC 960
Qy 955 ATAGAGACTCGCGTTATCCGAAGCCCGCATCTACTTGTATTTCTAGAACAACTTCAAT 1014
Db 961 ATAGAGGCTCGGTTATTAGGCTCGCATCTACTTGTATTTCCAGAACAGCTTACAAAT 1020
Qy 1015 TTTAGCACTTCATCAGATGGAGTGTCTACTAGGCAATATGACTTACTGGCGGGGCACACA 1074
Db 1021 TTCAGCGTATTAAAGTCGATGGAGTAATACTCAATATATGAAATTAAGTGGGACATAGA 1080
Qy 1075 ATTCAATCTCGGCCAATAGAGGCGGATTAATAATACCTCAACGATGGGTCTACCAATACT 1134
Db 1081 CTGGAATCGCGAACTAATAAGGGGGTCAATTAAGTACCTGGACACACGGAATACCAATACT 1140
Qy 1135 TCTATTAAATCCTGTAAGATTATCATTTCTCTCGAGACGTATATTGAGCTGAATCATAT 1194
Db 1141 TCTATTAAATCCTGTAAGATTATCATTTCTCTCGAGACGTATATTGAGCTGAATCATAT 1200
Qy 1195 GCAGGAGTCTTCTATAGGGGAATTTACCTTGAACCTTATTCATGGTGTCCCTACTGTAGA 1254
Db 1201 GCAGGAGTAAATAT-----ACTTCTAACTACTCTCTGTAATGGAGTACCTTTGGGCTAGA 1254
Qy 1255 TTTAATTTTAGGAACCTCAGATATCTTTTGAAGAGGTACTGCTAACTPATAGTCAACCC 1314
Db 1255 TTTAATTTGAGAAATCCCGTGAATCTCTT---AGAGGTAGCTTCTCTATACTATAGG 1311
Qy 1315 TATGAGTCACTGGGCTTCAATTTAAAGATTACAGAACTTCAAGAACTTACCACAGAAACA 1374
Db 1312 TATACGTGGAGTGGGACACACTATTTGATTCAGAACTGAATTTACCACAGAAACA 1371
Qy 1375 GAAACGACCAAAATATGAATCATATAGTCAATAGTTTATCTCAATAGGCTCAATTTCAAA 1434
Db 1372 GAAACGACCAAAATATGAATCTTACAGTCAATAGTTTATCTCAATAGGCTCAATTTCAAA 1431
Qy 1435 TCTAGGTCATGTACCAGTATTTCTGGACGACCGGTAGTGCAGATCGTCAAAATACC 1494
Db 1432 AACACTTTGAGAGCACCAATATTTCTGGACGACCGGTAGTGCAGATCGTCAAAATACC 1491
Qy 1495 ATTAGTTTCAGATAGCATACAAATATCCATTTGGTAAATCAATTCACCTTAATTCAGGT 1554
Db 1492 ATTAGTTTCAGATAGCATACAAATATCCATTTGGTAAATCAATTCACCTTAATTCAGGT 1551
Qy 1555 ACCTCTGTAGTCAGTGGCCAGGATTTTACAGAGGGGATATATCCGAACTAAACCTTAAT 1614
Db 1552 ACCTCTGTAGTCAGTGGCCAGGATTTTACAGAGGGGATATATCCGAACTAAACCTTAAT 1611
Qy 1615 GGTAGTGTACTAAGTATGGTCTTAAATTTTAAATAATACATATTAACAGGGTATCGCGTG 1674
Db 1612 GGTAGTGTACTAAGTATGGTCTTAAATTTTAAATAATACATATTAACAGGGTATCGCGTG 1671
Qy 1675 AGAGTTTCGTATGCTCTTCAAAATGTCCTGAGGGTAACTGTCGGAGGAGTACT 1734
Db 1672 AGAGTTTCGTATGCTCTTCAAAATGTCCTGAGGGTAACTGTCGGAGGAGTACT 1731
Qy 1735 ACTTTTGTATCAAGGATTCCTTAGTACTATGAGTGCAAATGAGTCTTTTGACATCTCAATCA 1794
Db 1732 ACTTTTGTATCAAGGATTCCTTAGTACTATGAGTGCAAATGAGTCTTTTGACATCTCAATCA 1791
Qy 1795 TTTAGATTTGCAAAATTTCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854
Db 1792 TTTAGATTTGCAAAATTTCTGTAGGTATTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1851

Qy 1855 AGTATAAGTAAATAATGACAGGTAGACAAACGTTTCACTTTTGATAAAAAATGAAATTCATTCCA 1914
Db 1852 AGTATAAGTAAATAATGACAGGTAGACAAACGTTTCACTTTTGATAAAAAATGAAATTCATTCCA 1911
Qy 1915 ATTACTCGAAGCTTCCGAAGCAGAAATACGATTTAGAAAAGGGCGCAAGAGCGGTGAATGCT 1974
Db 1912 ATTACTCGAAGCTTCCGAAGCAGAAATATGATTTAGAAAAGAGCGCAAGAGCGGTGAATGCT 1971
Qy 1975 CTGTTTACTAATACGAATCCGAAGAGATTGAAAACAGATGTGACAGATTTATCATTTGAT 2034
Db 1972 CTGTTTACTAATACGAATCCGAAGAGTTGAAAACAGGTGTGACAGATTTATCATTTGAT 2031
Qy 2035 CAAATGATCCAAATTTAGTGGCGTGTATTCGGAATGAATTCGCTTAGATGAAAAGAGAGAA 2094
Db 2032 GAAATGATCCAAATTTAGTGGCGTGTATTCGGAATGAATTCGCTTAGATGAAAAGAGAGAA 2091
Qy 2095 TTAATGAGAAAGTGAATATTCGAAAACGACTCAGTGTAGTGAAGAAAATTTACTCCAAAT 2154
Db 2092 TTAATGAGAAAGTGAATATTCGAAAACGACTCAGTGTAGTGAAGAAAATTTACTCCAAAT 2151
Qy 2155 CAAACTTTCATCCATCCATCAATAAGCAACGAGACTTCATATCTACTAATGAGCAATCGAAT 2214
Db 2152 CAAACTTTCATCCATCCATCAATAAGCAACGAGACTTCATATCTACTAATGAGCAATCGAAT 2211
Qy 2215 TTAATGAGAAAGTGAATATTCGAAAACGACTCAGTGTAGTGAAGAAAATTTACTCCAAAT 2274
Db 2212 TTAATGAGAAAGTGAATATTCGAAAACGACTCAGTGTAGTGAAGAAAATTTACTCCAAAT 2271
Qy 2275 CAGGAAGAAATGACGTAATTTAAAGAGAAATTAACGTACACTACCGGGGACTTTTAAATGAG 2334
Db 2272 CAGGAAGAAATGACGTAATTTAAAGAGAAATTAACGTACACTACCGGGGACTTTTAAATGAG 2331
Qy 2335 TGTATCCGAGTATTTATATCAAAAAATAGAGAGTCCGGAATTTAAAGCTTTATACTCGC 2394
Db 2332 TGTATCCGAGTATTTATATCAAAAAATAGAGAGTCCGGAATTTAAAGCTTTATACTCGC 2391
Qy 2395 TACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTAT 2454
Db 2392 TACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTGATTCGTTAT 2451
Qy 2455 AATCGAAACATGAAACATTCGATGTTCCAGGTACCGAGTCCGATGTCGCGCTTTCACTT 2514
Db 2452 AATCGAAACATGAAACATTCGATGTTCCAGGTACCGAGTCCGATGTCGCGCTTTCACTT 2511
Qy 2515 GAAAGCCCAATCGGAAGTGGGAGAACCGAATCGATCGGACCACTTTTGAATGGAAT 2574
Db 2512 GAAAGCCCAATCGGAAGTGGGAGAACCGAATCGATCGGACCACTTTTGAATGGAAT 2571
Qy 2575 CTTGATCTAGATTTGTTCTCGCAGAGATGGAAGAAATGTCGCAATCATTTCCCATCTTTC 2634
Db 2572 CTTGATCTAGATTTGTTCTCGCAGAGATGGAAGAAATGTCGCAATCATTTCCCATCTTTC 2631
Qy 2635 TCTTTGGATATTGATTTGGATGCAACAGACTTGCATGAGAAATCTAGGCGTGTGGGTGTA 2694
Db 2632 TCTTTGGATATTGATTTGGATGCAACAGACTTGCATGAGAAATCTAGGCGTGTGGGTGTA 2691
Qy 2695 TTAAGATTAAGACGAGGAAAGGTCAAGCAAGACTAGGGAATCTGGAATTTTATGAAGAG 2754
Db 2692 TTAAGATTAAGACGAGGAAAGGTCAAGCAAGACTAGGGAATCTGGAATTTTATGAAGAG 2751
Qy 2755 AAAACATTTATTAGGAGAGCACTGCTCGTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2814
Db 2752 AAAACATTTATTAGGAGAGCACTGCTCGTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2811
Qy 2815 AAACGTGAAAATCTAAATTTGAAAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2874
Db 2812 AAACGTGAAAATCTAAATTTGAAAACAAAACGAGTATATACAGAGGCAAAAGAGCTGTG 2871
Qy 2875 GATGCTTTATTGTTAGATTTCTCAATATATATAGATTTACAGCGGATACAAACATTTGGCATG 2934
Db 2872 GATGCTTTATTGTTAGATTTCTCAATATATATAGATTTACAGCGGATACAAACATTTGGCATG 2931

Db 711 TTAATGATGGTATATGCTCAAGCTGCAAAATTTACACCTATTATATATGAGATGCTCT 770
Qy 601 CTTTTTGGTAGTAAATTTGGGCTTACATCGCAGGAAATTCACGTTATATATGAGCGCCAA 660
Db 771 CTTTTTGGTAGTAAATTTGGGCTTACATCGCAGGAAATTCACGTTATATATGAGCGCCAA 830
Qy 661 GTGGAACAAACGAGAGATTAATCCGACTATATCGTAGAATGTAATAATACAGGTCTAAAT 720
Db 831 GTGGAACGAACGAGAGATTAATCCGACTATATCGTAGAATGTAATAATACAGGTCTAAAT 890
Qy 721 ACCTTGAGAGGACAAATCCGCAAGTTGGGTCGTTATATATCAATATTCGTHAGATCTA 780
Db 891 AGCTTGAGAGGACAAATCCGCAAGTTGGGTCGTTATATATCAATATTCGTHAGATCTA 950
Qy 781 ACCTTGAGGCTTATAGATCTAGTGGCACTATATCCCAAGCTATGACACTGCACTTATCCA 840
Db 951 ACCTTGAGGCTTATAGATCTAGTGGCACTATATCCCAAGCTATGACACTGCACTTATCCA 1010
Qy 841 ATAAATACGAGTCTCAGTTAA CAAGGGAAGTTTATACAGCGCAATTTGGAGCAACAGGG 900
Db 1011 ATAAATACGAGTCTCAGTTAA CAAGGGAAGTTTATACAGCGCAATTTGGAGCAACAGGG 1070
Qy 901 GTAATATGCGAAGTATGAATTTGGTATATAATATATATGACCTTCTGCTATAGAG 960
Db 1071 GTAATATGCGAAGTATGAATTTGGTATATAATATATATGACCTTCTGCTATAGAG 1130
Qy 961 ACTGCGGTTATCCGAAGCCGCACTACTTGTGATTTCTAGAACAACTTACAAATTTTACG 1020
Db 1131 GCTGCGGCTATCCGAAGCCGCACTACTTGTGATTTCTAGAACAACTTACAAATTTTACG 1190
Qy 1021 ACTTCATACGATGGAGTCTACTAGGCATATGACTTACTGCGGGGGGCAACAAATTCAA 1080
Db 1191 GCTTCATACGATGGAGTAACTACTAGGCATATGACTTACTGCGGGGGGCAACAGATTCAA 1250
Qy 1081 TCTCGGCCAATAGGAGGGGATTAATACCTCAACGATGGGTCTACCAATCTTCTATT 1140
Db 1251 TCTCGGCCAATAGGAGGGGATTAATACCTCAACGATGGGTCTACCAATCTTCTATT 1310
Qy 1141 AATCTGTAAAGATTAATCTTCTCTCGAGACGTTATTTGACCTGATCATATATGACGGA 1200
Db 1311 AATCTGTAAAGATTAATCTTCTCTCGAGACGTTATTTGACCTGATCATATATGACGGA 1370
Qy 1201 GTGCTTCTATGGGGAATTTACCTGAACTTCTCATGTGTCTCTACTGTTAGATTAAAT 1260
Db 1371 GTGCTTCTATGGGGAATTTACCTGAACTTCTCATGTGTCTCTACTGTTAGATTAAAT 1430
Qy 1261 TTTAGGAACCTCAGAAATCTTTTGAAGAGGTACTGTCTAATCTATAGTCAACCTTATGAG 1320
Db 1431 TTTAGGAACCTCAGAAATCTTTTGAAGAGGTAACGCTAATCTATAGTCAACCTTATGAG 1490
Qy 1321 TCACCTGGGCTTCAATTAAGATTCAGAACTGAAATACCAACAGAAACCAACAGACGA 1380
Db 1491 TCACCTGGGCTTCAATTAAGATTCAGAACTGAAATACCAACAGAAACCAACAGACGA 1550
Qy 1381 CCAAAATATGAATCATATAGTATAGGTTATCTCATAGAGGCTCATTTTCAAACTTAGG 1440
Db 1551 CCAAAATATGAATCATATAGTATAGGTTATCTCATATAGGTTAAATTTTACAACTCAGG 1610
Qy 1441 GTGCAATGATCAGATATATCTTGGAGGCAACCGTAGTGAGATCGTACAAATACCAATAGT 1500
Db 1611 GTGCAATGATCAGGATATATCTTGGAGGCAACCGTAGTGAGATCGTACAAATACCAATAGT 1670
Qy 1501 TCAGATAGCATAAACAAATACCAATGTTGTAATCATTTCAACCTTAAATTCAGGTACCTCT 1560
Db 1671 CCAAAATAGAAATCACCCAAATCCAAATGGTAAAGCATCCGAATTTCTTCAAGGTTACCACT 1730
Qy 1561 GTAGTCACTGGCCAGGATTTACAGGAGGGGATATAATCCGAATCAACGTTAAATGGTAGT 1620
Db 1731 GTTGTAGAGGACAGGATTTTACTGTTGGGATATCTTCTGAGAGCAACCAATCTGTTGGA 1790
Qy 1621 GTACTAAGTATGGGCTTAAATTTTAAATATACATCATTAACAGCGGTATCGCGTAGAGTT 1680

Db 1791 TTTGACCGATAAGAGTAACCTGTTAAACGAGCAATTAACACAAAGATATCGTATAGGATTC 1850
Qy 1681 CGTTATGCTGCTTCTTCAACCAATGCTCTGAGGGTAACTGTCGAGGAGGAGTACTACTTTT 1740
Db 1851 CGCTATGCTTCAACTGTAGATTTTGAATTTCTTTGTATCACGTGGAGGAGTACTGTAAT 1910
Qy 1741 GATCAAGGATTTCCCTTAGTACTATGAGTGCAAATAGTCTTTTGACATCTCAATCATTTAGA 1800
Db 1911 AATTTAGATTTCTTACGTACATGACAGTGGAGAGCAATTAATAACGAAATTTTGTG 1970
Qy 1801 TTTGAGAAATTTCTTGTAGGTAATAGTGCATCTGCGAGTCAA---ACTGCTGGAATAAGT 1857
Db 1971 AGACGTGCTTTTACTACACCTTTTACTTTTACAAATTTCAAGATATAATTCGAACGCT 2030
Qy 1858 ATAAAGTAATAATGCAAGGTAGCAACAGTTTCACTTTTGATAAAATTTGAATTTCAATTTCAAT 1917
Db 2031 AATCAAGGCTTTAGTGGAAATGGGGAAGTGTATATAGATAAAATTTGAATTTATTCAGTT 2090
Qy 1918 ACTGCAACCTTTGGAAGCAAAATACGATTTTGAAGGCGCAAGAGCGGTGAAATGCTCTG 1977
Db 2091 ACTGCAACCTTTGGAAGCAAAATATGATTTTGAAGAGCGCAAGAGCGGTGAAATGCTCTG 2150
Qy 1978 TTTACTAATACGAATCCGAAGAAGATTGAAACAGATGTGACAGATATCATTTGATCAA 2037
Db 2151 TTTACTAATACGAATCCGAAGAAGATTGAAACAGATGTGACAGATATCATTTGATCAA 2210
Qy 2038 GTATCCAATTTAGTGGGCTGTTTATCGGATCAATTTCTGCTTAGATGAAAGAGAGAAATTA 2097
Db 2211 GTATCCAATTTAGTGGGCTGTTTATCGGATCAATTTCTGCTTAGATGAAAGAGAGAAATTA 2270
Qy 2098 CTTGAGAAAGTGAATATTCGAAACGACTCAGTGATGAAAGAAAATTACTTCAAGATCCA 2157
Db 2271 CTTGAGAAAGTGAATATTCGAAACGACTCAGTGATGAAAGAAAATTACTTCAAGATCCA 2330
Qy 2158 AACTTCATCCATCAATTAAGCAACCGACTTCTATCTATCTATAGAGCAATTCGAATTC 2217
Db 2331 AACTTCATCCATCAATTAAGCAACCGACTTCTATCTATCTATAGAGCAATTCGAATTC 2390
Qy 2218 ACATCTATCCATGAACCAATCTGAACATGATGGGGAAGTGAGAAACATTTACATCCAG 2277
Db 2391 ACATCTATCCATGAACCAATCTGAACATGATGGGGAAGTGAGAAACATTTACATCCAG 2450
Qy 2278 GAAGGAAATGAGTATTTTAAAGAGAAATTAACGTCACACTACCGGGGACTTTTAAATGAGT 2337
Db 2451 GAAGGAAATGAGTATTTTAAAGAGAAATTAACGTCACACTACCGGGGACTTTTAAATGAGT 2510
Qy 2338 TATCGAGATTTTATATCAAAAAATAGGAGAGTGGGAATTTAAAGCTTATATCTCGCTAC 2397
Db 2511 TATCGAGATTTTATATCAAAAAATAGGAGAGTGGGAATTTAAAGCTTATATCTCGCTAC 2570
Qy 2398 CAATTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAT 2457
Db 2571 CAATTAAGAGGATATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGTTATAT 2630
Qy 2458 GCGAAAACATGAAACATTTGGATTTTCCAGGTAACCGAGTCCGATGCGGCTTTTCAAGTTGAA 2517
Db 2631 GCGAAAACATGAAACATTTGGATTTTCCAGGTAACCGAGTCCGATGCGGCTTTTCAAGTTGAA 2690
Qy 2518 AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGGACCAACATTTTGAATGGAATCCT 2577
Db 2691 AGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGGACCAACATTTTGAATGGAATCCT 2750
Qy 2578 GATCTAGATTTCTCTCGAGAGATGGGAAATATGTCGCATCATTTCCATCATTTCTCT 2637
Db 2751 GATCTAGATTTCTCTCGAGAGATGGGAAATATGTCGCATCATTTCCATCATTTCTCT 2810
Qy 2638 TTGGATATTTGATATTTGGATGACAGACTTGCATGAGAAATCTAGGCGTGGGTGATTC 2697
Db 2811 TTGGATATTTGATATTTGGATGACAGACTTGCATGAGAAATCTAGGCGTGGGTGATTC 2870
Qy 2698 AAGATTAAGACGCGAGGAGGTCTGCAAGACTAGGAAATCTGGAATTTTATTTGAAGAGAAA 2757
Db 2871 AAGATTAAGACGCGAGGAGGTCTGCAAGACTAGGAAATCTGGAATTTTATTTGAAGAGAAA 2930

Db 427 ATTGCTCGATTAGAAGGCTAGAGAGGCTATAGATCTTACCAGAGGCTCTTGAAACT 486
Qy 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTCTTTATACCCAAATATATAGCC 480
Db 487 TGGTTAGATAACCGAAATGATGCAAGATCAAGATCAAGACCAITTTCTTGAGCGCTATGTGCT 546
Qy 481 TTAGAACCTTGATTTCTTAATGGGATGCGCGCTTTTCGCAATTTAGAAAAACAGAAAGTTCCA 540
Db 547 TTAGAACCTTGATCTACTACTGCTATACCGCTTTTCAGAAATACGAAATGAAGAAGTTCCA 606
Qy 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTAATTTATGAGAGATGCTCT 600
Db 607 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTAATTTATGAGAGCGCATCC 666
Qy 601 CTTTTTGGTGTAGTGAATTTGGGCTTACATCGCAGGAAATTCACCGTTTATTTATGAGCGCCAA 660
Db 667 CTTTTTGGTGTAGTGAATTTGGGATGGCATCTTCCGATGTTAACCAATATTTACCAAGACAA 726
Qy 661 GTGGAAACAAACGAGAGATTTTCCGACTATTCGGTAGAATGGTATTAATACAGGTCTAAAT 720
Db 727 ATCAGATATACAGAGGAATTTCTAACCAATTCGCTACAAATGGTATTAATACAGGGCTAAAT 786
Qy 721 ACCTTTGAGAGGACAAATCCCAAGTTCGGTGGCTTAATCAATTCGCTAGAGATCTA 780
Db 787 AACTTTAAGAGGACAAATCTGAAGTGTGGTGGCTATAATCAATTCGCTAGAGACCTA 846
Qy 781 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
Db 847 ACGTTAGGGGTATTAGATTTAGTGGCTATTCCCAAGCTATGATGACTCGCACTTATCCA 906
Qy 841 ATAAATACGAGTCTCAGTTAAACAGGGAAAGTTTATACAGCGCAATTTGGAGCAACAGGG 900
Db 907 ATCAATACGAGTCTCAGTTAAACAGAGAAAATTTATACAGATCCCAATTTGGAGAAACAAAT 966
Qy 901 GTAAAT-----ATGCAAGTATGAATGGTATTAATTAATGCACTTCGTTTCCGCT 954
Db 967 GCACCTTCAGGAATTTGCAAGTACGAATGGTATTAATTAATGCACTTCGTTTCCGCT 1026
Qy 955 ATAGAGACTCGCGTTTATCGAAGCCGCACTACTTGTGATTTCTTAGAACAACTTACAAT 1014
Db 1027 ATAGAGGCTGCCATTTTCAGGCTCCGCACTACTTGTGATTTCCAGAACAACTTACAAT 1086
Qy 1015 TTTAGCACTTCAATCAAGTGGAGTGTACTAGGCAATGACTTACTGCGGGGGCACACA 1074
Db 1087 TACAGTGCATCAAGCGTTGGAGTAGCACTCAACATATGAATATTGTTGGTGGGACATAGG 1146
Qy 1075 ATTCATCTCGGCCAATAGGAGCGGATTAATACCTCAACCCATGGGTCTACCA---AT 1131
Db 1147 CTTAACTTCGGCCCAATAGGAGGACATTAATACCTCAACACAAAGGACTTACTAATAAT 1206
Qy 1132 ACTTCTATTAAATCCTGTAAAGTATATCATTTCTCTCGAGAGCTATATTGGACTGAATCA 1191
Db 1207 ACTTCAAATTAATCCTGTAAATACATGATTTAGCTTCGAGAGCTTTTAGAACAGATCA 1266
Qy 1192 TATCAGGAGTGTCTCTATGGGGAATTTACCTTGAACCTATTTCATGGTGTCCCTACTGTT 1251
Db 1267 AATCGAGGACAAATAT-----ACTATTACTCTCTGTGAATGGAGTACTTTGGGCT 1320
Qy 1252 AGATTTAATTTTAGAAACCTCAGAAATACTTTTGAAGAGGTPACTGTCTAACTATAGTCAA 1311
Db 1321 AGATTTAATTTTATAAACCTCAGAAATATTTATGAAGAGGGCGGCACCTACCTACAGTCAA 1380
Qy 1312 CCCTATGATGCTACCTGGGCTTCAATTTAAAGATTCAGAAATTCAGAAATACCACAGAAACA 1371
Db 1381 CGGTATCAGGAGTGTGGGATTCATTTATTTGATTCAGAAATTCAGAAATACCACAGAAACA 1440
Qy 1372 ACAGAACGACCAAAATATGAATCATATAGTCTATAGTGTATCTCACAATAGGGCTCATTTCA 1431
Db 1441 ACAGAACGACCAAAATATGAATCATATAGTCTATAGTGTATCTCATATAGGACTAATCATA 1500
Qy 1432 CAATCTAGGTGCTATGATCCAGTATATTTCTGGAGCGACCGTATGAGAGATGCTACAAAT 1491
Db 1501 GGAAACACCTTTGAGAGCACCACTTATTTCTTGGAGCGCATCGTAGTGCAGATCGTACGAAT 1560

Qy 1492 ACCATTTAGTTTCCAGATAGCATAAACAAATACCAATGGTAAAAATCAATTCAAACCTTAATTTCA 1551
Db 1561 ACGATTTGACCAAAATAGAAATTTACAAATACCAATGGTAAAAAGCACTGAATCTTCTATTTCA 1620
Qy 1552 GGTACTCTGTAGTCAAGTGGCCAGGATTTACAGAGGGGATATTAATCCGAACTAACGTT 1611
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Qy 1612 AATGTTAGTGTACTAAGTATGGTCTTAAATTTTAAATATACATCAATTCACAGGGTATCGC 1671
Db 1681 ACGGTACATTTGGAGATATACGATTAATATTAATGTGCCATTAATCCAAAGATATCGC 1740
Qy 1672 GTGAGAGTTCTGTATGTCTTCTCAAAACAAATGGTCTCGAGGGTAACTGTTCGAGGGAGT 1731
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Qy 1732 ACTACTTTTGTATCAAGGATTCCTAGTACTATGAGTGCAAATGAGTCTTTTGACATCTCAA 1791
Db 1801 ACTGTTAATATTTGTTAAATTTCTCAAGAACTATGAATAGGGGGATAATTTAGAAATATAGA 1860
Qy 1792 TCATTTAGATTTGAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAACTCTGGA 1851
Db 1861 AGTTTGAACCTGCAAGGATTTAGTCTCTTTTAAATTTTAAATGCCCCAAGCAATTC 1920
Qy 1852 ATAAAGTATAAGTAATAATGCAGGTAGACAAACGGTTTCACTTTGATAAAAAATGAAATTCAT 1911
Db 1921 ACATTTGGGTGCTCAGAGTTTTCAAATCAGGAAGTTTATATAGATAGAGTTCGAATTTGTT 1980
Qy 1912 CCAATTAATCTGCAACCTTCGAAAGCAATPAAGATTTAGAAAGGGGCAAGAGCGGTGAAT 1971
Db 1981 CCAGCAGAGGTAAACATTTGAGGCAAGATATGATTTAGAAAGAGACAAAGAGCGGTGAAT 2040
Qy 1972 GCTGTGTTACTAATACGAATCCAGAGATTTGAAACAGATGTGACAGATTTATCATTT 2031
Db 2041 GCTGTGTTACTTCTTACAAATCCAGAGATTTGAAACAGATGTGACAGATTTATCATTT 2100
Qy 2032 GATCAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGTTAGATGAAAAAGAGA 2091
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Qy 2152 GATCCAACTTCATCCATCAATTAAGCAACGACTTCATATCTACTAATGAGCAATCG 2211
Db 2221 GATCCAACTTCATCCATCAGTGGGCAATTTAAGTTTTCGATCCATCGTGGCAATCA 2280
Qy 2212 AATTTCACTCTATCCATGAACAAATCTGAACATGGATGGTGGGAGTGAAGCAATTA 2271
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Qy 2512 GTTGAAGCCCAATTCGAGAGTGGGAGAACCGGAATCGATGCGCACCAATTTTGAATGG 2571
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DB |||||
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DB |||||
QY 2632 TTCTCTTTGGATATTGATATTGGATGACAGACTTTCATGAGAAATCTAGGCGTGTGGGTG 2691
DB |||||
QY 2701 TTCATTGGATATTGATTTGGTGCACAGACTTTCATGAGAAATCTAGGCGTGTGGGTG 2760
DB |||||
QY 2692 GTATTCAAGATTAAAGACGCAAGAGTTCATGCAAGACTTAGGAAATCTGGAATTTATTGAA 2751
DB |||||
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DB |||||
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DB |||||
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DB |||||
QY 2992 TCTGTTATCCCGGTGTAAATCGGGAATTTTGAAGAAATTAGAAGTTCGCAATTTACCT 3051
DB |||||
QY 3061 CTTGTTATCCCGGTGTAAATCGGGAATTTTGAAGAAATTAGAAGTTCGCAATTTACCT 3120
DB |||||
QY 3052 GCAATCTCCCTATACGATCGGAGAAATGCTGTTAAATAATGTTGATTTTAATAATGATTA 3111
DB |||||
QY 3121 GCAATGCTCTTATACGATCGGAGAAATGCTGTTAAATAATGTTGATTTTAATAATGATTA 3180
DB |||||
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DB |||||
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DB |||||
QY 3172 GTTATCCAGAAATGGGAAGCAGAAATGTCTCAAGAGCGATTCGCTGTCTCGGGCGGTGGC 3231
DB |||||
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DB |||||
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DB |||||
QY 3301 TATATCTCTGTTGTCACAGGTACAAAGAGGATATGGAGAGGTTGTGTAAACGATCCAT 3360
DB |||||
QY 3292 GAAATCGAGAAATACAGAGCAACTAAAAATTTAAAAAATCTGTAAGAGAGGAGTGTAT 3351
DB |||||
QY 3361 GAAATCGAGAAATACAGAGCAACTAAAAATTTAAAAAATCTGTAAGAGAGGAGTGTAT 3420
DB |||||
QY 3352 CCAACCGGATACAGAAATGTAATGATTTATCTGCAACCAAGGTACAGCAGTATGTAAT 3411
DB |||||
QY 3421 CCAACCGGATACAGAAATGTAATGATTTATCTGCAACCAAGGTACAGCAGTATGTAAT 3480
DB |||||
QY 3412 TCCGTAATCTGATATGAGGATGCAATGAAATGATGATGATGATGATGATGATGATGATGAT 3471
DB |||||
QY 3481 TCCGTAATCTGATATGAGGATGCAATGAAATGATGATGATGATGATGATGATGATGATGAT 3540
DB |||||
QY 3472 AAACCGACTTATGAAGAGAAACGATATACAGATGTACAGAGAGATTAATCTGTGATAT 3531
DB |||||
QY 3541 AAACCGACTTATGAAGAGAAACGATATACAGATGTACAGAGAGATTAATCTGTGATAT 3600
DB |||||
QY 3532 GACAGAGGATGTGAATTTATCCACCACTACAGCTGTTTATATGACAAAAGAAATTAGAA 3591
DB |||||
QY 3601 GACAGAGGATGTGAATTTATCCACCACTACAGCTGTTTATGACAAAAGAAATTAGAA 3660
DB |||||
QY 3592 TACTTCCAGAAACCGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3651
DB |||||
QY 3661 TACTTCCAGAAACAGATACAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 3720
DB |||||
QY 3652 GTAGACAGCGTGGAAATTTACTCTCTTATGAGGAATAG 3687

DB 3721 GTAGATAGCTGGAACTACTCTCTCATGGAAGATAG 3756
|||||
RESULT 8
AAZ09160
ID AAZ09160 standard; DNA; 3932 BP.
XX AAZ09160;
AC AAZ09160;
XX
DT 18-OCT-1999 (first entry)
XX
DE B. thuringiensis cryET5 toxin DNA.
XX
KW Toxin; cryET4; cryET5; insecticidal; Lepidoptera; transformed plant;
KW crystal protein; insect; ds.
XX
OS Bacillus thuringiensis.
XX
PH Key Location/Qualifiers
FT CDS 67..3756
FT /*tag= a
FT /product= "cryET5"
FT /note= "No ATG start codon"
XX
XX US5942658-A.
PN
XX
PD 24-AUG-1999.
XX
PF 24-JUN-1997; 97US-00881340.
XX
PR 29-JUL-1993; 93US-00100709.
PR 30-DEC-1993; 93US-00176865.
PR 07-JUN-1995; 95US-00474038.
XX
XX (MONS) MONSANTO CO.
XX
XX Gonzalez JM, Jany CS, Tan Y, Donovan WP;
XX WPI; 1999-493544/41.
DR P-PSDB; AAY30923.
XX
XX Transformed plant comprising insecticidal crystal proteins.
PT
XX Claim 4; Fig 2A-J; 50pp; English.
PS
XX This invention describes novel transformed plants containing Bacillus
CC thuringiensis strain EG5847 insecticidal crystal protein genes cryET4 or
CC cryET5. cryET4 and cryET5 are novel toxin genes which produce
CC insecticidal proteins with activity against a broad spectrum of insects
CC of the order Lepidoptera. This sequence encodes the cryET5 protein
CC described in the method of the invention
XX
SQ Sequence 3932 BP; 1347 A; 650 C; 840 G; 1095 T; 0 U; 0 Other;
Query Match 72.9%; Score 2687.2; DB 2; Length 3932;
Best Local Similarity 83.5%; Pred. No. 0; Mismatches 593; Indels 15; Gaps 3;
Matches 3088; Conservative 0;
QY 1 TTGACTTCAAAATAGGAAAAATGAGAAATGAAATTTATAAATGCTTTATCGATTCCAGCTGTA 60
DB 67 TTGACTTCAAAATAGGAAAAATGAGAAATGAAATTTATAAATGCTTTATCGATTCCACGGTA 126
QY 61 TCGAATCATTTCCACACAAATGGATCTATCACCGAGTCTCGTATTGAGGATTTCTTTGTGT 120
DB 127 TCGAATCTCTCCACGCAAAATGAATCTATCACAGATGCTCGTATTGAAGATAGCTTTGTGT 186
QY 121 ATAGCCGAGGGGAATTAATATCAATCCACTTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
DB 187 GTAGCCGAGGTGAACAAATTTGATTCCTTTGTTAGCGCATCAACAGTCCAAACGGGTATA 246
QY 181 AACATAGCTGGTAGAATACTAGGTGATTAGGCGTACCGTTTCTCGACAAATAGCTTAGT 240
|||||

Db 247 AACATAGCTGTAGAAATTTGGGCGGTATTAGGTGTGCGGTTTGTGCGGCAACTAGCTAGT 306
Qy 241 TTTTATAGTTTCTTTGTTGGTAAATATATGGCCCGCGCAGAGATCACTGGGAAATTTTC 300
Db 307 TTTTATAGTTTCTTTGTTGGGAAATATATGGCCCTAGTGGCAGAGATCCATGGGAAATTTTC 366
Qy 301 CTAGAACATGTCGAACAATTTATAAATCAACAATAAACAAGAAATGCTAGGAATACGGCA 360
Db 367 CTGGAACATGTAGAACAACTTATAGACAACAACAAGTAAACAGAAAATPACTAGGAATACGGCT 426
Qy 361 CTTCGCTCGATTACAAAGTTTATAGAGATTCCTTTAGAGCCTATCAACAGTCACTTTGAAGAT 420
Db 427 ATTGCTCGATTAGAGAGGCTAGAGAGAGGCTATAGATCTTACCAGCAGGCTCTTGAAGACT 486
Qy 421 TGGCTAGAAAACCGTGATGATGCAAGAACGAGAAAGTTTCTTTATACCCAATATATAGCC 480
Db 487 TGGTTAGATACCGAAATGATGCAAGATCAAGAACATTTCTTGAGCGGCTATGTTGCT 546
Qy 481 TTAGAACTTGATTTCTTAATGCGGATGCGCTTTTTCGCAATVAGAAAACAAGAGTTCCA 540
Db 547 TTAGAACTTGATTTCTTAATGCGGATGCGCTTTTTCGCAATVAGAAAACAAGAGTTCCA 606
Qy 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTATTTAGAGAGTGCCTCT 600
Db 607 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTATTTAGAGAGCGCATCC 666
Qy 601 CTTTTTGGTGTAGTAAATTTGGGCTTACATCGCAGGAAATTTCAACGTTATTATGAGCGCAA 660
Db 667 CTTTTTGGTGTAGTAAATTTGGGCTTACATCGCAGGAAATTTCAACGTTATTATGAGCGCAA 726
Qy 661 GTGGAACAAACGAGAGATTTATTCGACTATTGCGTATGATGATGATGATGATGATGATGAT 720
Db 727 ATCAGATATACAGAGGAATTTCTAAACATTCGATGATGATGATGATGATGATGATGATGAT 786
Qy 721 AGCTTGAGAGGACAAATCCCGCAGATTTGGGTGCGGTATATCAATTCCTGATGATGATGAT 780
Db 787 AACTTAAGAGGACAAATTCGTAAGTTGGTTGGGTGCGGTATATCAATTCCTGATGATGATGAT 846
Qy 781 ACGTTAGGGGTATTAGATCTAGTGCACCTATTCCCAAGCTATGACACTCGCACTTATCCA 840
Db 847 ACGTTAGGGGTATTAGATCTAGTGCACCTATTCCCAAGCTATGACACTCGCACTTATCCA 906
Qy 841 ATAATACGAGTGTCTCAGTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGG 900
Db 907 ATCAATACGAGTGTCTCAGTTAAACAGGGAAGTTTATACAGATCCAAATTTGGAGCAACAA 966
Qy 901 GTAAT-----ATGGCAAGTATGAATTTGGTATATATATATATATATATATATATATATAT 954
Db 967 GCACCTTCAGGATTTGCAAGTACGAAATTTGGTTTATATATATATATATATATATATATATAT 1026
Qy 955 ATAGAGACTGCGGTTATCCGAAGCCCGCATCTACTTGTATTTCTAGAACAACTTACAAAT 1014
Db 1027 ATAGAGGCTGCCATTTTACGGCTCCGATCTACTTGTATTTTCCGAACAACCTTACAAAT 1086
Qy 1015 TTTAGCACTTCATCAACGATGGAGTGTCTACTAGGCATATGACTTACTGCGGGGGGCACACA 1074
Db 1087 TACAGTGATCAAGCCGTTGGAGTAGCACTCAACATATGAATTTATTTGGTGGGACATAGG 1146
Qy 1075 ATTCAATCTCGGCCAATAGAGGCGGATTAATATCTCAACGATGGGTCTACCA---AT 1131
Db 1147 CTTAACCTTCCGCCAATAGAGGAGCAATTAATATCTCAACAGCAAGCACTTACTAATAAT 1206
Qy 1132 ACTTCTATTAATCCGTAGATATATCTTCTCTCGAGAGGTATATTTGAGCTGAAATCA 1191
Db 1207 ACTTCAATTAATCCGTAGATATATCTTCTCTCGAGAGGTATATTTGAGCTGAAATCA 1266
Qy 1192 TATGAGGAGTGTCTTCTATGGGAAATTTTACCTTGAAACCTATTCTATGGTGTCCCTACTGTT 1251
Db 1267 AATGAGGAGCAAAATAT-----ACTATTTACTACTCTCTGTGAATGGAGTACTTGGGCT 1320
Qy 1252 AGATTTAATTTAGGAACCCCTCAGAAATATCTTTTGAAGAGGTTACTGCTTAATATAGTCAA 1311
Db 1321 AGATTTAATTTTATAACCCCTCAGAAATATTTATGAAGAGGCGCCACTTACTACAGTCAA 1380

Qy 1312 CCCTATAGTCACTCGGCTTCAAATTAAGAAATCAGAAAATGAAATACCAACAGAAACA 1371
Db 1381 CCGTATCAGGAGTTGGGATTCATTAATTTGATTCAGAACTGAATTTACCAACAGAAACA 1440
Qy 1372 ACAGAACGACCAAAATTAATGAATCATATAGTCATATAGTTTATCTCATATAGGCTCATTTCA 1431
Db 1441 ACAGAACGACCAAAATTAATGAATCATATAGTCATATAGTTTATCTCATATAGGACTAATCATA 1500
Qy 1432 CAATCTAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1491
Db 1501 GGAACACTTTTGAGAGCACCAAGTCTATTTTGGAGCGCATCTAGTGGCAGATCGTACGAAT 1560
Qy 1492 ACCATTAGTTCAGATAGCATAAACAAATACCAATTTGGTAAATCATTTCAACTTTAAATTTCA 1551
Db 1561 ACGATTGGACCAATAGAAATTAACAAATACCAATTTGGTAAAGCACTGAATCTTTCATTTCA 1620
Qy 1552 GGTACCTCTGTAGTACGTGGCCAGGATTTACAGAGAGGAGATATAATCCGAACTAAACGTT 1611
Db 1621 GGTGTACTGTGTTGGAGGGCCAGGATTTACAGGTGGGATATCTCTCGTAGAACAAAT 1680
Qy 1612 AATGCTAGTGTACTAAGTATGGGTCTTAATTTTAAATTAATATACATCATATACAGGCTATCGC 1671
Db 1681 ACGGTACATTTGGAGATATACGAATTAATTAATTTAGTCCATTTATCCAAAGATATCGC 1740
Qy 1672 GTGAGAGTTCTGTATGCTTCTCAACCAATGCTCTGAGGGTAACTGTCCGAGGAGT 1731
Db 1741 GTAAGGATTCGTTATGCTTCTACTACAGATTTACAATTTTTCACAGAAATTAATGGAACC 1800
Qy 1732 ACTACTTTTGTATCAAGGATTCCTTAGTACTATAGTGCAGAAATAGTCTTTGACATCTCAA 1791
Db 1801 ACTGTAAATATGTTAAATTTCTCAAGAACTATGAATAGGGGGGATTAATTTAGAAATATAGA 1860
Qy 1792 TCATTTAGTTTTCAGAAATTTCTGTAGTATTTAGTGCATCTGGCAGTCAACCTGCTGGA 1851
Db 1861 AGTTTGTAGACTGAGGATTTAGTACTCTCTTTTAAATTTTAAATGCCCCAAGCACATTC 1920
Qy 1852 ATAAGTATTAAGTAAATTAATGAGGTAGCAACAGTTTCTCACTTTGATTAATTTGAAATTCAT 1911
Db 1921 ACATTTGGGTCTCAGAGTTTTCAAATCAGGAGTTTATATAGATAGTGCATTTGTT 1980
Qy 1912 CCAATTACTGCAACCTTTGAAAGCAGAAATACGAATTTAGAAAGGGCGCAAGCGCGTGAAT 1971
Db 1981 CCAGCAGAGGTAAACATTTGAGGCGAGAAATATGATTTAGAAAGCAGCAAAAAGCGCGTGAAT 2040
Qy 1972 GCTCTGTTTACTAATACGAATCCAAAGAGATTGAAACAGATGTGACAGATATATCATATT 2031
Db 2041 GCTCTGTTTACTTCTACAAATCCAAAGAGATTGAAACAGATGTGACAGATATATCATATT 2100
Qy 2032 GATCAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGTTAGATGAAAGAGA 2091
Db 2101 GACCAAGTGTCCAATATGTTGGCATGTTTATCAGATGAATTTGCTTGGATGAGAGCGA 2160
Qy 2092 GAATTTACTTGAGAAAGTGAATATTCGAAACGACTCAGTGTATGAAAGAAACCTTACTCCAA 2151
Db 2161 GAATTTTGGAAAGTGAATATTCGAAAGCGACTCAGTGTATGAAAGAAACCTTACTCCAA 2220
Qy 2152 GATCCAACTTTCACATCCATCAATAAGCAACGACTTTCATATCTATATGAGCAATCG 2211
Db 2221 GATCCAACTTTCACATTCATCAGTGGGCAATTAATAGTTTTCGATCCATCGATGGCAATCA 2280
Qy 2212 AATTTTCACTCTTCATGCAACATCTGAACATGATGGTGGGAGGTGAGAAACATTTACA 2271
Db 2281 AACTTCCCTCTTATTAATGAGCTATCTGAACATGATGGTGGGAGGTGCGAATGTTTACC 2340
Qy 2272 ATCCAGGAAGGAAATGACGTAATTTTAAAGAGAAATTCGTCACACTACCGGGGACTTTTAAAT 2331
Db 2341 ATTCCAGGAAGGAGTACGTAATTTTAAAGAGAAATTCGTCACACTACCGGGGACTTTTAAAT 2400
Qy 2332 GAGTGTATTCGAGCTATTTATATCAAAAAATAGGAGGTGCGAATTTTAAAGCTTTTACT 2391
Db 2401 GAGTGTATTCGAAATTTTATATCAAAAAATAGGAGGTGCGAATTTTAAAGCTTTTACT 2460

2392 CGCTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2451
Db |||||
2461 CGCTATCAATTAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2520
Qy |||||
2452 TATAATCGAAACATGAAACATTGGATGTTCCAGGTACCGAGTCCGATGCGCGCTTCA 2511
Db |||||
2521 TACAATCGAAAGCATGAAACATTGGATGTTCCAGGTACCGAGTCCGATGCGCGCTTCA 2580
Qy |||||
2512 GTTGAAGCCCAATCGAAGGTGCGGAGAACCGAATCGATGCCACACATTTTGAATGG 2571
Db |||||
2581 GTTGAAGCCCAATCGAAGGTGCGGAGAACCAAAATCGATGCCACACATTTTGAATGG 2640
Qy |||||
2572 AATCCTGATCTAGATTTCTCTCGAGATGGAGAAAATGTCGCATCATTTCCCATCAT 2631
Db |||||
2641 AATCCTGATCTAGATTTCTCTCGAGATGGAGAAAATGTCGCATCATTTCCCATCAT 2700
Qy |||||
2632 TTCTCTTTGGATATTGATATTGGATGCACAGCTTGCATGAGAATCTAGCGGTGCGGTG 2691
Db |||||
2701 TTCACCTTGGATATTGATTTGGTGCACAGACTTGCATGAGAACCTAGCGGTGCGGTG 2760
Qy |||||
2692 GTATTCAAGATTAAAGCGGAGGAGTTCATGCAAGACTAGGGAATCTGGAAATTTATGAA 2751
Db |||||
2761 GTATTCAAGATTAAAGCGGAGGAGTTCATGCAAGATTAGGAAATCTGGAAATTTATCGAA 2820
Qy |||||
2752 GAGAAACCAATTATTAGGAGAACACTGCTCTCGTGTGAAGAGACAGAGAAAATCGAGA 2811
Db |||||
2821 GAGAAACCAATTATTAGGAGAACACTGCTCTCGTGTGAAGAGACAGAGAAAATCGAGA 2880
Qy |||||
2812 GACAAAGCTGAAACACTACAAATTTGGAACAAAACGAGTATATACAGAGCAAAAAGAGCT 2871
Db |||||
2881 GACAAAGCTGAAACACTACAAATTTGGAACAAAACGAGTATATACAGAGCAAAAAGAGCT 2940
Qy |||||
2872 GTGGATGCTTTATTTCTAGATTTCTCAATATAATAGATTCAACGCGATACAAATGCGC 2931
Db |||||
2941 GTGGATGCTTTATTTCTAGATTTCTCAATATAATAGATTCAACGCGATACAAATGCGC 3000
Qy |||||
2932 ATGATTCATCGCGCAGATAAATTTGTTTCATCGAATTCGAGAGCTTATCTGTGAGAAATTA 2991
Db |||||
3001 ATGATTCATCGCGCAGATAAATTTGTTTCATCGAATTCGAGAGCTTATCTTTCAGAAATTA 3060
Qy |||||
2992 TCTGTTATCCCGGTGTAATGCGGAAATTTTGAAGAAATTAGAAGTCGCAATTCACCT 3051
Db |||||
3061 CCTGTTATCCCGGTGTAATGCGGAAATTTTGAAGAAATTAGAAGTCGCAATTCACCT 3120
Qy |||||
3052 GCATCTCCCTATACGATCGGAGAAATGCTGTTAAATGCTGATTTTAAATGATTA 3111
Db |||||
3121 GCAATGCTCTTATACGATCGGAGAAATGCTGTTAAATGCTGATTTTAAATGATTA 3180
Qy |||||
3112 GCATGCTGGAATGTAAGGGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCTT 3171
Db |||||
3181 ACATGTTGGAATGTAAGGGCATGTAGATGTACAACAGAGCCATCATCTGTTCTGACCTT 3240
Qy |||||
3172 GTTATCCAGAAATGGGAAGCAGAAGTGTCAACAGCAGTTCGCGTCTGTCGCGGCGGTGGC 3231
Db |||||
3241 GTTATCCAGAAATGGGAAGCAGAAGTGTCAACAGCAGTTCGCGTCTGTCGCGGCGGTGGC 3300
Qy |||||
3232 TATATCTCCTGCTCACAGGTCACAAGAGGGATATGGAGGGTGTGTGAAGCATCCAT 3291
Db |||||
3301 TATATCTCCTGCTCACAGGTCACAAGAGGGATATGGAGGGTGTGTGAAGCATCCAT 3360
Qy |||||
3292 GAAATCGAGAAACAAATACAGACGAATTAATAATTTAAATCTGTGAAGAGGAAGTGTAT 3351
Db |||||
3361 GAAATCGAGAAACAAATACAGACGAATTAATAATTTAAATCTGTGAAGAGGAAGTGTAT 3420
Qy |||||
3352 CCAACGGATACAGGAACGTTAATGATATATATGTCACACCAAGGTACAGCAGTATGTAAT 3411
Db |||||
3421 CCAACGGATACAGGAACGTTAATGATATATATGTCACACCAAGGTACAGCAGTATGTAAT 3480
Qy |||||
3412 TCCCGTAAATGCTGATATGAGGATGCATATGAAGTTGATCTACAGCATCTGTTAATAC 3471
Db |||||
3481 TCCCGTAAATGCTGATATGAGGATGCATATGAAGTTGATCTACAGCATCTGTTAATAC 3540
Qy |||||
3472 AAACCGACTTTATGAAGAGAAACGTTATACAGATGTACGAGAGATAATCATTTGTGAATAT 3531

Db ||||| 3541 AAACCGACTTTATGAAGAGAAACGTTATACAGATGTACGAGAGATATCATTTGTGAATAT 3600
Qy ||||| 3532 GACAGAGGTATGTGAATTTATCCACACTACACAGCTGGTTATATGACAAAAAGAAATTAGAA 3591
Db ||||| 3601 GACAGAGGTATGTGAATTTATCCACAGTACACAGCTGGTTATGTGACAAAAAGAAATTAGAA 3660
Qy ||||| 3592 TACTTCCCAGAACCGATAGGTTAGATTGGAGTGGAGAACCGAGGAGGATTATT 3651
Db ||||| 3661 TACTTCCCAGAACAGATACAGTATGATTGGAGATTGGAGAACCGAGGAGGATTATT 3720
Qy ||||| 3652 GTAGACAGCTCGAAATTTACTCTCTTATGGAGGAATAG 3687
Db ||||| 3721 GTAGATAGCTGGAATCTCTCTCATGGAGGAATAG 3756

RESULT 9
AAT95051
ID AAT95051 standard; DNA; 3934 BP.
XX AAT95051;
XX DT 17-FEB-1998 (first entry)
XX DNA encoding Bacillus thuringiensis crystal toxin CryET5.
DE EG7283; crystal toxin; CryET5; lepidopteran pest; Lymantria dispar;
KW Ostrinia nubilalis; Pseudoplusia includens; Plutella xylostella;
KW Spodoptera exigua; Spodoptera frugiperda; Trichoplusia ni; ds.
XX Bacillus thuringiensis.
XX Key Location/Qualifiers
FT CDS 67..3756
FT /*tag= a
FT /product= "CryET5"
XX US5679343-A.
XX 21-OCT-1997.
XX 07-JUN-1995; 95US-00474038.
XX 29-JUL-1993; 93US-00100709.
XX 30-DEC-1993; 93US-00176865.
XX (MONS) MONSANTO CO.
XX PI Jany CS, Gonzalez JM, Donovan WP, Tan Y;
XX WPI; 1997-525882/48.
XX P-PSDB; AAW35259.
XX Lepidopteran toxic Bacillus thuringiensis crystal protein - useful to control Lepidopteran pests.
XX Example 2; Fig 2; 50pp; English.
XX The present sequence encodes the Bacillus thuringiensis EG7283 crystal toxin CryET5, which, optionally in association with B. thuringiensis EG7283, can be used against lepidopteran pests. CryET5 is especially useful for controlling Lymantria dispar, Ostrinia nubilalis, Pseudoplusia includens, Plutella xylostella, Spodoptera exigua, Spodoptera frugiperda and Trichoplusia ni
XX SQ Sequence 3934 BP; 1347 A; 650 C; 841 G; 1096 T; 0 U; 0 Other;
Query Match 72.9%; Score 2687.2; DB 2; Length 3934;
Best Local Similarity 83.5%; Pred No. 0;
Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;
Qy 1 TTGACTTCAATAGGAAAAATGAGAAATGAAATTTATAAATGCTTTATCGATTCCAGCTGTA 60
|||||

Db 67 TTGACTTCAATAGGAAATAGAGAAATGAAATATAAAATGCTTTATCGATTCCAAAGGTA 126
Qy 61 TCGAATCATTTCCACAAATGATCTATCACCAGATGCTCGTATTGAGGATCTTTGTGT 120
Db 127 TCGAATCTTCCACGCAATGATCTATCACCAGATGCTCGTATTGAGGATGCTTTGT 186
Qy 121 ATAGCGGAGGGAATTAATCAATCACTTTGTTAGGGAATCAACAGTCCAAACGGGTATT 180
Db 187 GTAGCGGAGGTGAACAATATTGATCCATTTGTTAGGCAATCAACAGTCCAAACGGGTATA 246
Qy 181 AACATAGCTGGTAGAATACTAGTGTATTAGGCGTACCGTTGCTGGACAAATAGCTAGT 240
Db 247 AACATAGCTGGTAGAATAATTGGCGGTATTAGGTTGCGGTATTTGCTGGCAACTAGCTAGT 306
Qy 241 TTTTATAGTTTCTTGTGGTGAATATGCGCCCGCGGACAGATCAGTGGGAAATTTTC 300
Db 307 TTTTATAGTTTCTTGTGGGAAATATGCGCTAGTGGGAGATCCATGGGAAATTTTC 366
Qy 301 CTAGAACATGTGCAACAACTTATAAATCAACAAATAACAGAAATGCTAGGAAATACGGCA 360
Db 367 CTGGAAACATGTAGAACAACTTATAAGACAAACAGTAAACAGAAATACGGCT 426
Qy 361 CTGCTCGATTACAGGTTTAGGAGATTCCTTTAGAGCTTATCAACAGTCACTTGAAGAT 420
Db 427 ATTGCTCGATTAGAAAGGCTTAGGAAAGAGGCTATAGATCTTACAGCAGGCTCTTGAAACT 486
Qy 421 TGGCTAGAAACCGTGATGATCAAGAACGAGAGTGTCTTTATACCCAAATATATAGCC 480
Db 487 TGGTTAGATACCGAAATGATGCAAGATCAAGAGCATTTTCTTGAGGCTATGTTGCT 546
Qy 481 TTAGAACTTGATTTCTTAATCGAGTCCGCTTTTTCGCAATTTAGAAACCAAGAGTTCCA 540
Db 547 TTAGAACTTGATTTCTTACTACTGCTATACCGCTTTTTCGAAATACGAAATGAGAGTTCCA 606
Qy 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTTATTTATTTAGAGATGCTCT 600
Db 607 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTTATTTATTTAGAGAGACCATCC 666
Qy 601 CTTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAAATTTCAAGTATTATTAGAGGCCAA 660
Db 667 CTTTTTGGTAGTGAATTTGGGAGTGCATCTCCGATGTTAACCAATATTACAGAACAA 726
Qy 661 GTGGAAACAAACGAGAGATTTATTCGACTATTGCGTAGAATGGTATAATACAGGCTTAAAT 720
Db 727 ATCAGATATACAGAGAAATTTCTAACCATTCGCTACAAATGGTATAATACAGGCGTAAAT 786
Qy 721 AGCTTGAGAGGGAACAAATGCCCAAGTTGGGTCGCTTATATCAATTTCCGTAGAGATCTA 780
Db 787 AACTTAAAGAGGGAACAAATGCTGAAAGTTGGTTGCGGTATAATCAATTTCCGTAGAGACCTA 846
Qy 781 ACGTTAGGGGTATTAGATCTAGTGCACATTTCCCAAGCTATGACACTCGCACTTTATCCA 840
Db 847 ACGTTAGGGGTATTAGATTTAGTAGCCCTATTTCCCAAGCTATGATCTCGCACTTTATCCA 906
Qy 841 ATAAATACGAGTGTCTCAGTTTAAACAGGGAAGTTTATACAGAGCAATTTGGAGCAACAGGG 900
Db 907 ATCAATACGAGTGTCTCAGTTTAAACAGAGAAATTTATACAGATCCAAATTTGGGAGCAAAAT 966
Qy 901 GTAAAT-----ATGCGAAGTATGAATTTGGTATAATTAATATGACACTTCGTTTCCGCT 954
Db 967 GCACCTTCAGGATTTGCAAGTACGAATTTGGTTTAAATAATATGCAACCATCGTTTTCGCC 1026
Qy 955 ATAGAGACTCGGGTTATCGAAGCCCGCATCTACTTGTATTTCTTAGAACAACTTACAAT 1014
Db 1027 ATAGAGGCTCGCAATTTTCAAGGCTCCGCACTACTTGTATTTTCCAGAACAACTTACAAT 1086
Qy 1015 TTTAGCACTTCACTACGATGGAGTGTCTACTAGGCAATATGACTTACTGCGGGGGGACACA 1074
Db 1087 TACAGTGCATCAAGCGTTGGAGTAGCACTCAACATATGAATTTATTTGGTGGGACATAGG 1146
Qy 1075 ATTCAATCTCGGCCAATAGGAGCGGGAATTAATACCTCAACGCAATGGGTCTACCA---AT 1131
Db 1147 CTTAACTTCCGCCAATAGGAGGGAATTAATAATACCTCAACAGGACTTACTAATTAAT 1206

Qy 1132 ACTTCTATTAAATCCTGTAAGATTATCAATTTCTTCTCGAGACGTATATTGGACTGAATCA 1191
Db 1207 ACTTCAATTAATCCTGTAACATTACAGTTTACGTTCTCGAGACGTTTATAGAACAGATCA 1266
Qy 1192 TATGAGAGTGTCTTCTATGCGGAATTTTACCTTGAAOCTTATTTATGTTGCTCTACTGTT 1251
Db 1267 AATGAGGGAACAAATAT-----ACTATTTACTACTCTCTGTAATGAGTAGTACTTTGGGCT 1320
Qy 1252 AGATTTAATTTTGGAAACCTCTCAGAACTATTTTGAAGAGGTAAGTCTTAACTATAGTCAA 1311
Db 1321 AGATTTAATTTTAAACCCCTCAGAAATTTTATGAAGAGGCGCACCTACCTACAGTCAA 1380
Qy 1312 CCCTATAGTCACTCTGGGCTTCAATTTAAAGATTCAGAAATTCGAATTAACCAACAGAAACA 1371
Db 1381 CCGTATCAGGAGTTGGGATTTCAATTTATTTGATTGAGAACTGGAATTAACCAACAGAAACA 1440
Qy 1372 ACAGAACGACCAAAATTTATGAATCATATAGTCAATAGGTTTATCTCATATAGGCTCATTTCA 1431
Db 1441 ACAGAACGACCAAAATTTATGAATCATATAGTCAATAGTATTTCTCATATAGGACTAATCATA 1500
Qy 1432 CAATCTAGGCTGCATGTACAGTATATTTCTTTGGAGCGCACCGTAGTGCAGATCGTACAAT 1491
Db 1501 GGAACACTTTTGGAGGACCCAGTCTTATTTTGGAGCGCATCGTAGTGCAGATCGTACGAAT 1560
Qy 1492 ACCATTAGTTTCCAGATAGCATAAACAAATACCATTTGGTAAATATCAATTCACCTTAAATCA 1551
Db 1561 ACGATTGACCAATAGNATTTACAAATACATTTGGTAAAGCACTGAAATTTCTTCAATCA 1620
Qy 1552 GGTACTCTGTAGTCAAGTCCAGGATTTTACAGAGGGGATATAATCCGAACATAACGTT 1611
Db 1621 GGTGTACTGTGTTGGAGGCGCAGGATTTACAGTGGGGATATCTCTCGTAGAACAAAT 1680
Qy 1612 AATGGTAGTGTACTAAGTATGCGTCTTAATTTTAAATATACTATCATCATACAGCGGTATCGC 1671
Db 1681 ACGGATACATTTGGAGATATACGATTAATTAATTAATGTGCCATTTATCCAAAGATATCGC 1740
Qy 1672 GTGAGAGTTCGTTATGCTGCTTCTCAACAAATGCTCTGAGGTAATCTGTCGAGGAGT 1731
Db 1741 GTAGGATTCGTTATGCTTCTACTACAGATTTACATTTTTCACGAGATTAATGGAACC 1800
Qy 1732 ACTACTTTTGTATCAAGGATTCCTTAGTACTATAGTGCAAATAGAGTCTTTTGACATCTCAA 1791
Db 1801 ACTGTTAATATGGTAAATTTCTCAAGAACTATGAATAGGGGGATAATTTTGAATATAGA 1860
Qy 1792 TCATTTAGATTTGAGAAATTTCTGTTAGTATTTAGTGCATCTGGCAGTCAAACTGCTGA 1851
Db 1861 AGTTTGAACCTGAGGATTTAGTACTCTCTTTTAAATTTTAAATGCCCNAAGCAATTC 1920
Qy 1852 ATAAAGTATAAGTAAATTAATGCAGGTAGACAAACGTTTCACTTTGATAAAATTTGAATTCAT 1911
Db 1921 ACATTTGGGTGCTCAGAGTTTTCAAATCAGGAAGTTTATATAGATAGAGTCGAATTTGTT 1980
Qy 1912 CCAATTAATGCAACCTTCGAAAGCAGAAATACGATTTAGAAAGGGCGCAAGAGCGGTGAAT 1971
Db 1981 CCAGCAGAGGTAAACATTTGAGGCGAATAATGATTTAGAAAGAGCAACAAAGCGGTGAAT 2040
Qy 1972 GCTCTGTTTACTAATACGAATCCAAAGATTTGAAACAGATGTGACAGATTTATCATATT 2031
Db 2041 GCTCTGTTTACTTCTTCAAAATCCAAAGAGATTTGAAACAGATGTGACAGATTTATCATATT 2100
Qy 2032 GATCAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATTTCTGCTTAGATGAAAGAGA 2091
Db 2101 GACCAAGTGTCCAATATGGTGGCATGTTTATCAGATGAATTTTGTGCTGATGAGAGCGA 2160
Qy 2092 GAAATTTACTTGAGAAAGTGAATATTCGAAACGACTCAGTGTATGAAAGAACTTACTCAA 2151
Db 2161 GAAATTTACTTGAGAAAGTGAATATTCGAAAGCGACTCAGTGTATGAAAGAACTTACTCAA 2220
Qy 2152 GATCCAAACTTCACTCCATCAATTAAGCAACGACTTCAATCTACTAATAGAGCAATCG 2211
Db 2221 GATCCAAACTTCACTCCATCAATTAAGTGGGCAATTAAGTGGTTCGATCCATCGATGGAGCAATCA 2280

Qy	2212	AATTTTCACTATCTCCATGAAACAATCTGTAAACATCGATGGTGGGGAAGTGAGAACATTTACA	2271
Db	2281	AACTTCCCCTCTATTAAATGAGCTATCTGAAACATGGATGGTGGGGAAGTGCGAATGTTTACC	2340
Qy	2272	ATCCAGGAAGGAAATGACGTATTTTAAAGAGAAATTCGTCACATACCGGGGACCTTTTAAT	2331
Db	2341	ATTGAGGAGGGATGACGCTATTTTAAAGAGAAATTCGTCACATACCGGGTACTTTTAAAT	2400
Qy	2332	GAGTGTATTCCGACGCTATTTTATATCAAAAAATAGGAGAGTCGGAAATTTAAAGCTTATPACT	2391
Db	2401	GAGTGTATTCCAAAATATTATTTATATCAAAAAATAGGAGAGTCAGAAATTTAAAGCTTATPACG	2460
Qy	2392	CGCTACCAATTTAAGAGGGTATATTGGAAGATAGTCAAGATTTAGAGATATATTGATTCCT	2451
Db	2461	CGCTATCAATTTAAGAGGGTATTTTGAAGATAGTCAAGATCTAGAGATTTATTAAATTCGT	2520
Qy	2452	TATTAATCGAAACAATGAACAATTTGGATGTTTCCAGGTACCGAGTCGGTATCGCCGCTTTTCA	2511
Db	2521	TACAAATGCMAAGCATGAAACATTTGGATGTTTCCAGGTACCGATTTCCCTATGGCCGCTTTCA	2580
Qy	2512	GTTCAAAAGCCCAATCGGAAGTGGCGGAGAACCGAATCGATGCGCACACAATTTTGAATGG	2571
Db	2581	GTTGAAAGCCCAATTCGAAGTGGCGGAGAACCAAAATCGATCGCACACAATTTTGAATGG	2640
Qy	2572	AATCCTGATCTAGATTTGTTCTCGCAGAGATGGAGAAAAATGTGGCATCATCTCCCATCAT	2631
Db	2641	AATCCTGATCTAGATTTGTTCTCGCAGAGATGGAGAAAGTGTGGCATCATTTCCCATCAT	2700
Qy	2632	TTCTCTTTGGATATGTGATATTTGGATGCACAGACTTGTGCATGAGAAATCTAGGCGTGGGTG	2691
Db	2701	TTCACTTTGGATATGTGATTTGGGTGGCACAGACTTGCATGAGAACCCTAGGCGTGGGTG	2760
Qy	2692	GTATTTCAAGATTTAAGACGCGAGGAGGTCATGCAAGACTAGGGAATCTGGAAATTTATTGAA	2751
Db	2761	GTATTTCAAGATTTAAGACGCGAAGGTTATGCAAGATTTAGAAATCTGGAAATTTATCGAA	2820
Qy	2752	GAGAAACCATTTATTAGGAGAAGCACTCTCTGTTGGAAGAGAGCAGAGAAAAAATGAGAGA	2811
Db	2821	GAGAAACCATTTAATTGGAAGACACTGCTCTGTTGGAAGAGAGCGGAAAAAATAATGAGAGA	2880
Qy	2812	GACAAACGTCGAAAACTTCAATTTGGAACCAAAACGAGTATATACAGAGCCAAAAGAGCT	2871
Db	2881	GACAAACGGA AAAAATCAATTTGGAACCAAAACGAGTATATACAGAGCCAAAAGAGCT	2940
Qy	2872	GTGGATGCTTTATTTGTAGATTTCTCAATATAATAGATTTACAAGCGGATACAAACATTTGCG	2931
Db	2941	GTGGATGCTTTATTCGTAGATTTCTCAATATGATCAATTTACAAGCGGATACAAACATTTGCG	3000
Qy	2932	ATGATTCATCGGCAGATAAATCTGTTTATCGAAATTCGAGAGGCTTATCTGTACAGAAATTA	2991
Db	3001	ATGATTCATCGGCAGATAAATCTGTTTATCGAAATTCGAGAGGCTTATCTTTTACAGAAATTA	3060
Qy	2992	TCTGTTATCCGGGTGTAAATGCGGAAATTTTGAAGAAATTAGAAGGTCGCATTTATCACT	3051
Db	3061	CCTGTTATCCAGGTGTAAATGCGGAAATTTTGAAGAAATTAGAAGGTCACATTTATCACT	3120
Qy	3052	GCAATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGGTGAATTTTAATAATGGAATTA	3111
Db	3121	GCAATGTCCTTATACGATGCGAGAAATGTCGTTAAAAATGGTGAATTTTAATAATGGAATTA	3180
Qy	3112	GCATGCTGGAATGTAAAAAGGCAATGATAGATGTAACAACAGAGCCATCACCGTCTGTGCCCTT	3171
Db	3181	ACATGTTGGAAATGTAAAAAGGCAATGATAGATGTAACAACAGAGCCATCATCGTCTGTGACCTT	3240
Qy	3172	GTTATCCAGAAATGGGAAGCAGAAAGTGTCAACAAGCTTCCGCTCTGTCCGGGGCGTGGC	3231
Db	3241	GTTATCCAGAAATGGGAAGCAGAAAGTGTCAACAAGCTTCCGCTCTGTCCGGGGCGTGGC	3300
Qy	3232	TATATCTCTCGTGTCAAGCGTCAAGAGGGATATGGAGAGGGTGTGTGTAAACGATCCAT	3291
Db	3301	TATATCTCTCTGTGTCAAGCGTCAAGAGGGATATGGAGAGGGTGTGTGTAAACGATCCAT	3360
Qy	3292	GAAATCGAGAACAAATACAGACGAATTAATAATTTAAAAAATCTGTGAAGAGAGGAAGTGTAT	3351

Db	3361	GAATTCGAGAACAAATACAGACGAACATAAAATTTAAAACTGTGAGAGAGAGGAAGTGAT	3420
Qy	3352	CCAACGGATACAGGACGAGCTGTATGATTATCTACGACACCCAGGTACACGATGATGTAAT	3411
Db	3421	CCAACGGATACAGGACGAGCTGTATGATTATCTACGACACCCAGGTACAGCATGTAAT	3480
Qy	3412	TCCCGTAATCTGGATATGAGGATGTCATATGAAGTTGATACACGATCTGTTAATTAC	3471
Db	3481	TCCCGTAATCTGGATATGAGGATGTCATATGAAGTTGATACACGATCTGTTAATTAC	3540
Qy	3472	AAACCGACTTATCAAGAGAAACGTTATACAGATGTACGAGAGATATCATTTCTGGAATAT	3531
Db	3541	AAACCGACTTATCAAGAGAAACGTTATACAGATGTACGAGAGATATCATTTCTGGAATAT	3600
Qy	3532	GACAGAGGGTATGTGAATTATCCACCACCTACACGATGCGTTATATGACAAAAGAAATTAGAA	3591
Db	3601	GACAGAGGGTATGTGAATTATCCACCACCTACACGATGCGTTATATGACAAAAGAAATTAGAA	3660
Qy	3592	TACTTCCGAAACCCGATAGGATGATGGATGAGATTGGAGAAAACGGAAGGAAGTTTATT	3651
Db	3661	TACTTCCGAAACCCGATAGGATGATGGATGAGATTGGAGAAAACGGAAGGAAGTTTATT	3720
Qy	3652	GTAGACAGCGTGGAAATTACTCTTATGGAGGAATAG	3687
Db	3721	GTAGATAGCGTGGAAATTACTCTTATGGAGGAATAG	3756
RESULT 10			
AAT68434			
ID 68434 standard; DNA; 3934 BP.			
XX	AC	AAT68434;	
XX	AC	AAT68434;	
DT	25-MAR-2003	(revised)	
DT	07-JUL-1997	(first entry)	
XX	XX		
DE	CryET5 gene.		
XX	XX		
KW	CryET5; cryET4; Bacillus thuringiensis; insecticidal crystal protein;		
KW	ICP; toxin; CryI protein; lepidopteran insect; insecticide; db.		
XX	Bacillus thuringiensis.		
XX	XX		
FH	Key	Location/Qualifiers	
FT	CDS	67..3756	
FT		/*tag= a	
FT		/product= "cryET5"	
XX	US5616319-A.		
XX	XX		
PD	01-APR-1997.		
XX	XX		
PF	30-DEC-1993;	93US-00176865.	
XX	XX		
PR	29-JUL-1993;	93US-00100709.	
XX	XX		
PA	(MONS) MONSANTO CO.		
XX	XX		
PI	Gonzalez JM, Donovan WP, Tan Y, Jany CS;		
XX	XX		
DR	WPI; 1997-212077/19.		
DR	P-PSDB; AAWI7699.		
XX	XX		
PT	Bacillus thuringiensis cryET5 gene encoding insecticidal protein - useful		
XX	for control of lepidopteran pests.		
XX	XX		
PS	Claim 2; Fig 2; 50pp; English.		
XX	XX		
CC	This sequence represents the cryET5 gene of Bacillus thuringiensis (B.t.)		
CC	isolate EG5847. B.t. produces inclusions during sporulation which include		
CC	insecticidal crystal proteins (ICP). ICP toxins are active in insects		
CC	only after ingestion. Once ingested, the toxic components disrupt the		

CC midgut cells, resulting in cessation of feeding, and eventually death.
CC The CryI proteins produced by B.t. are active against lepidopteran
CC insects. The protein encoded by this sequence, and the CryE4 protein
CC (see AAW17700) belong to the CryI family of ICPs. This sequence can be
CC used to transform bacteria, which are useful as insecticides against a
CC wide range of lepidopteran pests, and can be applied to crops, soil and
CC seeds. The encoded protein, or especially its toxic N terminal region,
CC can be expressed in plants, to provide protection against lepidopteran
CC pests. This sequence, or its fragments, can also be used to isolate other
CC similar genes. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ

Sequence 3934 BP; 1347 A; 650 C; 841 G; 1096 T; 0 U; 0 Other;

Query Match 72.9%; Score 2687.2; DB 2; Length 3934;

Best Local Similarity 83.5%; Pred. No. 0;

Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

Qy	1	TTGACCTTCAATAGAGAAAATAGAAATGAAATATAAATGCTTTATCGATTCCAGCTGTA	60
Db	67	TTGACCTTCAATAGAGAAAATAGAAATGAAATATAAATGCTTTATCGATTCCAGCTGTA	126
Qy	61	TGCAATCATTCACACAAATGATCTATCACCAGATGCTCGTATTGAGGATCTTTGTGT	120
Db	127	TGCAATCCTTCCACCAATGAAATCTATCACCAGATGCTCGTATTGAAATGATGCTTTGT	186
Qy	121	ATAGCCGAGGGGAATATATCAATCCACTTGTAGCGCATCAACAGTCCAAACGGGTATT	180
Db	187	GTAGCCGAGGTGAACAAATATTGATCCATTTGTAGCGCATCAACAGTCCAAACGGGTATA	246
Qy	181	AACATAGCTGGTAGAATCTAGTGTAATAGGCGTACCGTTTGTGGCAAAATAGCTAGT	240
Db	247	AACATAGCTGGTAGAATATGGGCGTATATAGGTGTGCGGTTTGTGGCAAACTAGCTAGT	306
Qy	241	TTTTATAGTTTCTTGTGGTGAATATATAGGCGGCGGCGGAGATCACTGGGAAATTTTC	300
Db	307	TTTTATAGTTTCTTGTGGGGAATATATAGGCGGCGGCGGAGATCCATGGGAAATTTTC	366
Qy	301	CTAGAACATGTGCAACAACTTATAAATCAACAAATAACAGAAATGCTAGGAATACGGCA	360
Db	367	CTAGAACATGTAGAACAACTTATAGACAAACAGTAAACAGAAATGCTAGGAATACGGCT	426
Qy	361	CTTGCTCGAATACAAAGTTTAGGAGATTCCTTTAGAGCGCTATCAACAGTCACTGAAGAT	420
Db	427	ATTGCTCGAATAGAAAGTCTAGGAGAGGCTATAGATCTTACCAGCGCTCTTGAAACT	486
Qy	421	TGGCTAGAAACCGTGATGATGCAAGACGAGAGTGTCTTTATACCAATATATAGCC	480
Db	487	TGGTTAGATAACCGAAATGATGCAAGATCAAGAGCATTAATCTTGAGCGCTATGTTGCT	546
Qy	481	TTAGAACTTGATTTTCTTAATGCGATGCGCTTTTCGCAATTTAGAAACCAAGAGTTCCA	540
Db	547	TTAGAACTTGATTTTCTTAATGCGATGCGCTTTTCGCAATTTAGAAACCAAGAGTTCCA	606
Qy	541	TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTAATTTATGAGAGATGCTCT	600
Db	607	TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATTAATTTATGAGAGATGCT	666
Qy	601	CTTTTGGTGTAGTATTTGGGCTTATCAGCGAGGAAATCAACGTTATATGAGCGCCAA	660
Db	667	CTTTTGGTGTAGTATTTGGGCTTATCAGCGAGGAAATCAACGTTATATGAGCGCCAA	726
Qy	661	GTGGAACAAACGAGAGATTTATTCGCAATTTATGCGTAGAATGGTATAATACAGGTTCAAT	720
Db	727	ATCAGATATACAGAGGAATATTTCAACCAATTTGCGTACAAATGGTATAATACAGGCTAAT	786
Qy	721	AGCTTAGAGGGGACAAATGCCCGAAGTTGGGTGGGTTAATCAATTCCTCGTAGAGATCTA	780
Db	787	AACTTAAGAGGGACAAATGCTGAAAGTTGGTTGGGTATTAATCAATTCCTCGTAGAGATCTA	846
Qy	781	ACGTTAGGGGTATTAGATCTAGTGGCACTATTTCCAGCTATGACATCGGCACTTATCCA	840
Db	847	ACGTTAGGGGTATTAGATTTAGTGGCCCTATTTCCAGCTATGATCTCGCACTTATCCA	906

Qy	841	ATAAATACAGTGTCTCAGTTAAACAGGAAGTTTATACAGACGCAATTTGGAGCAACAGG	900
Db	907	ATCAATACAGTGTCTCAGTTAAACAGGAAGTTTATACAGATCCAAATTTGGAGCAACAAAT	966
Qy	901	GTAAAT-----ATGGCAAGTATGAATGGTATTAATAATATATGCACTTCGTTTCCGCT	954
Db	967	GCACCTTCAGGATTTGCAAGTACGAATTTGGTTTAAATAATAATGCAACCATCGTTTCTGCC	1026
Qy	955	ATAGAGCTGGGTATTCGGAAGCCGATCTCTGATTTGATTTTCTAGACAACTTCAATTT	1014
Db	1027	ATAGAGCTGGCATTTTTCAGGCTCCGATCTCTCTGATTTTTCAGAAACAACTTCAATTT	1086
Qy	1015	TTTAGCACTTCATCAAGATGAGTGTCTACTAGGATATGATCTACTGGCGGGGACACACA	1074
Db	1087	TACAGTGCATCAAGCCGTTGGAGTAGCACTCAACATATGAATTTATGGTGGGACATAGG	1146
Qy	1075	ATTCAATCTCGGCAATAGGAGGGGATTAATACCTCAACGATGGGTCTACCA---AT	1131
Db	1147	CTTAACCTTCGCCCAATAGGAGGGGACATTAATAATACCTCAACAGAGGACTTACTAATAAT	1206
Qy	1132	ACTTCTATTAATCTGTAAAGATTATCAATCTCTCTCGAGAGCTATATTGGACTGAATCA	1191
Db	1207	ACTTCAATTAATCTGTAAACATTAAGTTTACGTTTACGTTCTCGAGAGCTTTATAGAACAGAATCA	1266
Qy	1192	TATGAGAGTGTCTTCTATGGGGAATTTTACCTTGAACCTTATTCATGGTGTCCCTACTGTT	1251
Db	1267	ATGAGGAGCAAAATAT-----ACTATTTACTACTCTCTGTAATGGAGTACTTGGGCT	1320
Qy	1252	AGATTTAATTTTGAAGACCCCTCAGAATACTTTTGAAGAGGTACTGTCTTAACTATAGTCAA	1311
Db	1321	AGATTTAATTTTAAACCCCTCAGAATACTTTTGAAGAGGCGGCACCTACCTACAGTCAA	1380
Qy	1312	CCCTATGAGTCACTGGGCTTCAATTAAGATTTCAAGAACTGAAATTTACCAACAGAAACA	1371
Db	1381	CCGTTATCAGGAGTTGGGATTTCAATTTTGAATTCAGAAACTGAAATTTACCAACAGAAACA	1440
Qy	1372	ACAGAAACCAAAATTAATGATCATATAGTCTATAGTCTTCTCATAGGCTCTCAATTTCA	1431
Db	1441	ACAGAAACCAAAATTAATGATCATATAGTCTATAGTCTTCTCATATAGGCTCTCAATTTCA	1500
Qy	1432	CAATCTAGGTTGATGTAACAGTATACTTTGGAACGACCGTAGTGCAGATCGTACAAAT	1491
Db	1501	GGAAACACTTTTGAGAGCACCACTCTATTTCTTGGACGCACTCGTAGTGCAGATCGTACGAAT	1560
Qy	1492	ACCAATAGTTCAGATGATTAACCAATACCAATTTGGTAAATCTTCTTAACTTAAATTTCA	1551
Db	1561	ACGAATGGACCAAAATAGAAATTTACCAAAATACCTTTGGTAAAGCACTGAATCTTCAATTTCA	1620
Qy	1552	GGTACCTCTGTAGTCACTGGCCAGGATTTTACAGAGGGGATATAATCCGAACTAAACGTT	1611
Db	1621	GGTGTACTTGTGTGGAGGGCCAGGATTTTACAGGTGGGATATCTCTTCTGTAGAACAAAT	1680
Qy	1612	AATCGTATGTAATTAAGTATGGGCTTTAATTTTAAATAATACATCATTTACAGCGGTATCGC	1671
Db	1681	ACGGGTACATTTGAGATATACGAATTAATAATTAATGTCCATTTATCCAAAGATATCGC	1740
Qy	1672	GTGAGATTCGTTATGCTTCTTCAACAAATGCTCTGAGGGTAACTGTGCGAGGGAGT	1731
Db	1741	GTAAGGATTCGTTATGCTTCTTACTACAGATTTAACAATTTTTCACAGGAATTAATGGAAC	1800
Qy	1732	ACTACTTTTGAATCAAGGATTCCTCTAGTATGATGCAAAATGAGTCTTTTGACATCTCAA	1791
Db	1801	ACTGTTAATTTGTTAATTTCTCAAGAACTATGAATAGGGGGGATTAATTTAGATATAGA	1860
Qy	1792	TCATTTAGATTTGAGAAATTTCTGTAGTATTAATGATCTGCGAGTCAAACTGCTGGA	1851
Db	1861	AGTTTAAAGACGTCAGGATTTAGTACTCTTTTAAATTTTAAATGCCCAGCAACATTC	1920
Qy	1852	ATAAGTATAGTATTAATGAGGTAGACAAACGTTTCACTTTGATTAATAATTTGAATTTCA	1911
Db	1921	ACATTTGGGTGCTCAGAGTTTTCAAATTCAGGAAGTTTATATAGATAGAGTTCGAATTTGTT	1980
Qy	1912	CCAATTTACTGCAACCTTCGGAAGCAGAAATACGATTTTGAAGGGCGGCAAGCGGTGAAT	1971

1981 CCAGCAGAGGTAACTTTGAGGCGAGAAATATGATTTAGAAAGAGCACAAGGCGGTGAAT 2040
1972 GCTCTGTTTACTTAATACGAATCCAGAGATTCAGAAACAGATGTGACAGATATCATATT 2031
2041 GCTCTGTTTACTTCTCAAAATCCAGAGATTCAGAAACAGATGTGACAGATATCATATT 2100
2032 GATCAAGATATCCAAATTTAGTGGCGTGTATCGGATGAATTCCTGTAGATGAAGAGAGA 2091
2101 GACCAAGTTCCTAATATGTTGGCAATGTTATCAGATGAATTTGCTGTGATGAGAGCGA 2160
2092 GAAATTAATTTAGAAAGTGAATAATCGAAACGATCGATGATGAAGAAACTTTACTCCAA 2151
2161 GAATTAATTTAGAAAGTGAATAATCGAAACGATCGATGATGAAGAAACTTTACTCCAA 2220
2152 GATCCAAACTTCACATCCATCAATAGCAACAGACTTCATATCTACTAATGAGCAATCG 2211
2221 GATCCAAACTTCACATCCATCAATAGCAACAGACTTCATATCTACTAATGAGCAATCA 2280
2212 AATTTCCACATCTATCCATGAACAACTCTGAACATGGATGGTGGGAAAGTGAGAACATTACA 2271
2281 AACTTCCCTCTAATTAATGAGCTATCTGAACATGGATGGTGGGAAAGTGCGAATGTTACC 2340
2272 ATCCAGAGAGAAATGACGTATTTAAGAGAATTACGTCACACTACCGGGGACTTTTAAAT 2331
2341 ATTCCAGAGAGAAATGACGTATTTAAGAGAATTACGTCACACTACCGGGGACTTTTAAAT 2400
2332 GAGTGTTATCCGAGGTATTTATATCAAAAATAGGAGAGTCGGAATTAAGAGCTTATACT 2391
2401 GAGTGTTATCCAAATTTATATATCAAAAATAGGAGAGTCAGAAATTAAGAGCTTATACG 2460
2392 CGCTACCAATTAAGAGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2451
2461 CGCTATCAATTAAGAGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2520
2452 TATAATGCGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGATGCGCGCTTCA 2511
2521 TACAATGCGAAACATGAAACATTTGGATGTTCCAGGTACCGATTCCTATGGCGCGCTTCA 2580
2512 GTTGAAGCCCAATCGGAAGGTCGGAGACCGAATCGATGCGCACACATTTTGAATGG 2571
2581 GTTGAAGCCCAATCGGAAGGTCGGAGAACCAAAATCGATGCGCACACATTTTGAATGG 2640
2572 AATCCTGATCTAGATTTGTTCTCGCAGAGATGGAGAAAATGTGCGCATCATATCCCATCAT 2631
2641 AATCCTGATCTAGATTTGTTCTCGCAGAGATGGAGAAAGATGTGCGCATCATATCCCATCAT 2700
2632 TTCTCTTTGGATATTTGATATTTGATGACAGACTTGATGATGAGAAATCTAGCGCGTGGGTG 2691
2701 TTCACTTTGGATATTTGATGTTGGGTGACAGACTTGATGATGAGAACTTAGCGGTGGGTG 2760
2692 GTATTCAAGATTAAGACGCGAGGAGTTCATGCAAGACTAGGGAATCTGGAATTTATTGAA 2751
2761 GTATTCAAGATTAAGACGCGAGGAGTTCATGCAAGATTAAGAAATCTGGAATTTATCGAA 2820
2752 GAGAAACCATTTATGAGAGAGCACTGCTCGTGTGAAGAGAGCAGAGAAAAAATGAGAG 2811
2821 GAGAAACCATTTATGAGAGAGCACTGCTCGTGTGAAGAGAGCGGAAAAAATGAGAG 2880
2812 GACAAAACGTGAAAACTCAATTTGGAAACAAAACGAGTATATACAGAGCGGAAAAAGAGCT 2871
2881 GACAAAACGTGAAAACTCAATTTGGAAACAAAACGAGTATATACAGAGCGGAAAAAGAGCT 2940
2872 GTGGATGCTTTATTTGTAGATTCTCAATATATAGATTTACAGCGGATACAAACATTGGC 2931
2941 GTGGATGCTTTATTTGTAGATTCTCAATATATAGATTTACAGCGGATACAAACATTGGC 3000
2932 ATGATTCATGCGGAGATAAACTTTGTTCAATCGAATTCGAGAGGCTTATCTGTCAAGATTA 2991
3001 ATGATTCATGCGGAGATAAACTTTGTTCAATCGAATTCGAGAGGCTTATCTTCAAGATTA 3060
2992 TCTGTATATCCCGGTGTAATGCGGAAATTTTGAAGAAATTAGAAGGTGCGATTATCACT 3051

3061 CCTGTTATCCAGGTGTAAATGCGGAAATTTTGAAGAAATTTAGAAAGTGCACATTTCACT 3120
3052 GCAATCTCCCTATACGATGCGAGAAATCTCGTTAAAAATGTTGATTTTAAATATGATTA 3111
3121 GCATGTCCTTATACGATGCGAGAAATCTCGTTAAAAATGTTGATTTTAAATATGATTA 3180
3112 GCATGTCGGAATGTAAAAAGGCGATGTAGATGTACAAAGAGCCATCACGGTCTGTCCCTT 3171
3181 ACATGTTGGAATGTAAAAAGGCGATGTAGATGTACAAAGAGCCATCATCGTCTGACCTT 3240
3172 GTTATCCAGAAATGGAAGAGCAAGGTGTCAAGCAGTTCCGCTCTGTCCGGGCGTGCG 3231
3241 GTTATCCAGAAATGGAAGAGCAAGGTGTCAAGCAGTTCCGCTCTGTCCGGGCGTGCG 3300
3232 TATATCTCTCCGCTGTCAAGCGGTACAAAGAGGATATGAGAGGGTGTGTAAACGATCCAT 3291
3301 TATATCTCTCGTGTCAAGCGGTACAAAGAGGATATGAGAGGGTGTGTAAACGATCCAT 3360
3292 GAAATCGAGAAACAATACAGACGAACTAAAAATTTAAAACTGTGAAGAGAGGAAGTGTAT 3351
3361 GAAATCGAGAAACAATACAGACGAACTAAAAATTTAAAACTGTGAAGAGAGGAAGTGTAT 3420
3352 CCAACGGATACAGGAACCGTGTAAATGATTAATCTGCACACCAAGGTACAGCATGTGTAAAT 3411
3421 CCAACGGATACAGGAACCGTGTAAATGATTAATCTGCACACCAAGGTACAGCATGTGTAAAT 3480
3412 TCCCTGTAATGCTGGATATGAGGATGCATATGAAGTTGATCTACAGCATCTGTAAATTAAC 3471
3481 TCCCTGTAATGCTGGATATGAGGATGCATATGAAGTTGATCTACAGCATCTGTAAATTAAC 3540
3472 AAACCGACTTATGAAGAGAAACCGTATACAGATGTACGAAGAGATAATCATTTGTGAATAT 3531
3541 AAACCGACTTATGAAGAGAAACCGTATACAGATGTACGAAGAGATAATCATTTGTGAATAT 3600
3532 GACAGAGGTATGTGAATTTATCCACCTACCAGCTGGTTATATGACAAAAAATTAGAA 3591
3601 GACAGAGGTATGTGAATTTATCCACCTACCAGCTGGTTATATGACAAAAAATTAGAA 3660
3592 TACTTCCCAAGAACCGATTAAGGTATGGAATTTGAGATTGGAGAAACGGAAGGAGTTTATT 3651
3661 TACTTCCCAAGAACCGATTAAGGTATGGAATTTGAGATTGGAGAAACGGAAGGAGTTTATT 3720
3652 GTAGACAGCGTGAATTTACTCTTATGGAGGAATAG 3687
3721 GTAGATAGCGTGAATTTACTCTCTCATGGAGGAATAG 3756

RESULT 11

AAV83927
ID AAV83927 standard; DNA; 3934 BP.

XX

AC AAV83927;

XX

DT 03-MAR-1999 (first entry)

XX

DNA encoding a CryET5 protein.

DE

CryET4; Bacillus thuringiensis strain EG5847; crystal toxin; CryET5;

Lepidoptera; Helicoverpa zea; resistant strain; Plutella xylostella;

Spodoptera exigua; S. frugiperda; S. frugiperda; Trichoplusia ni; ds.

XX

Bacillus thuringiensis.

XX

Key Location/Qualifiers

67..3756

FT CDS

FT /*tag= a

FT /product= "CrtET5"

XX

US5854053-A.

PN

XX

29-DEC-1998.

PD

XX

06-JAN-1997; 97US-00779046.

Db	1741	GTAAAGGATTCGGTTATGCTTCTACTACAGATTTTACAATTTTTTCACGAGAA'TTAATGTGAACC	1800
Qy	1732	ACTACTTTTTGATCAAGGATTCCTCTAGTACTATAGATGCAAA'TGAGTCTTTTGA'CATCTCAA	1791
Db	1801	ACTGTTAATATTTGGTAATTTCTCAAGAAC'TATGAATAGGGGGGATAA'TTTAGAAATATAGA	1860
Qy	1792	TCATTTAGATTTGCAGAAATTTCTGTAGGTATTTAGTGCATCTGGCAGTCAAA'CTGCTGGA	1851
Db	1861	AGTTTTAGAACTGCAGGATTTAGTACTCTTTTAA'TTTTAAATGCCAAAGCAATTC	1920
Qy	1852	ATAAGTATAAGTATAATATGCAGGTAGACAAACGTTTTCAC'TTGTATAAAA'TTGAATTCATTT	1911
Db	1921	ACATTTGGTGCTCAGAGTTTTTCAAATCAGGAAGTTTATATAGATAGAGT'CGAAATTTGTT	1980
Qy	1912	CCATTTACTCCAACTTCGAGCAGATACGATTTTAGAAAGGGCGCAAGAGCGGTGNAAT	1971
Db	1981	CCAGCAGAGTAACTTTTGAGGCAGAAATATGATTTTAAAAAGAGCA'AAAAAGGCGGTGAAT	2040
Qy	1972	GCCTCTGTTTACTAATACGAATCCAAAGAAGATTTGAAAACAGATGTGCAGAGATTTATCATATTT	2031
Db	2041	GCTCTGTTTACTTCTACAAATCCAAAGAAATTTGAAAACAGATGTGCAGAGATTTATCATATTT	2100
Qy	2032	GATCAAGTATCCAAATTTTAGTGGCGTGTTTATCGGA'TGAATTTCTGTTTATGATGAAAAAGAGA	2091
Db	2101	GACCAAGTGTCCAAATATGTTGGCATGTTTATCAGATGAA'TTTTGTCTGGATGAGAAGCGA	2160
Qy	2092	GAATTACTTCGAGAAAGTGAATATGCGAAGCACTCAGTGCATGATGAAAGAACTTTACTCCAA	2151
Db	2161	GAATTTATTTGAGAAAGTGAATATGCGAAGCGACTCAGTGCATGATGAAAGAACTTTACTCCAA	2220
Qy	2152	GATCCAACTTTCACATCCATCAATTAAGCAACAGACTTTCA'TATCTACTAATGAGCAATCG	2211
Db	2221	GATCCAACTTTCACATTCATCAGTGGGCATTTAAGTTTCGA'TTCCATCCATCGATGACAAATCA	2280
Qy	2212	AATTTCACTCTATCCATGAACAATCTGAACATGGATGGTGGGGAAGTGAGAACATTTACA	2271
Db	2281	AACTTCCCTCTATTAATGAGCTATCTGAACATGGATGGTGGGGAAGTGCAGATTTTACC	2340
Qy	2272	ATCCGAAAGGAATGACGTTATTTAAAGAGAAATACGTCA'CACTACCGGGGACTTTTAAAT	2331
Db	2341	ATTGAGGAAGGGAATGACGTTATTTAAAGAGAAATTA'CGTCA'CACTACCGGGTACTTTTAAAT	2400
Qy	2332	GAGTGTATTCCGAGCTATTTATATCAAAAAATAGGAGAGT'CGGAA'TTAAAGGCTTATACT	2391
Db	2401	GAGTGTATTCAAATTTATTTATATCAAAAAATAGGAGAGT'GAGAA'TTTAAAGGTTTATACG	2460
Qy	2392	CGCTACCAATTAAGAGGGTATTTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT	2451
Db	2461	CGCTATCAA'TTAAAGAGGGTATATTGAAGATAGTCAAGATCTAGAGATTTATTTAAATTCGT	2520
Qy	2452	TATAATCGGAAA'CAATGAAA'CAATTTGGATGTTTCCAGGTTACCGAGTCCGATATGGCCGCTTCA	2511
Db	2521	TACAAATGCAAGCATGAAA'CAATTTGGATGTTTCCAGGTTACCGATTTCCCTATATGGCCGCTTCA	2580
Qy	2512	GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAA'TCGATCGCACCA'CAATTTTGAATGG	2571
Db	2581	GTTGAAAGCCCAATCGGAAGGTGCGGAGAACCGAA'ATCGATCGCACCA'CAATTTTGAATGG	2640
Qy	2572	AATCCTGATCTAGATTTGTTCTTCGAGAGATGAGAAAAAAT'TGTCGCATCATTTCCCATCAT	2631
Db	2641	AATCCTGATCTAGATTTGTTCTTCGAGAGATGAGAAAAAAT'TGTCGCATCATTTCCCATCAT	2700
Qy	2632	TTCTCTTTTGATATTTGATATTTGATGCACAGACTTGTGATGAGAA'TCTAGGCGTGTGGGTG	2691
Db	2701	TTCACTTTTGATATTTGATTTGTTGGGTGCACAGACTTGTGATGAGAA'CCCTAGGCGTGTGGGTG	2760
Qy	2692	GTATTCAGATTTAAGCGCAGGAGGTCATGCAAGACTAGGGAATCTAGGGAATCTTGAATTTATGAA	2751
Db	2761	GTATTCAGATTTAAGCGCAGGAGGTTATGCAAGATTTAGGAATCTGGAATCTTATTCGAA	2820
Qy	2752	GAGAAACCA'TTATTTAGGAGAGCACTGCTCTGTTGTAAGAGAGCAGAGAAAAAATGGAGA	2811

Db	2821	GAGAAACCATTTAAATTGGAGAAAGCACTGTCTCGTGTGAAGAGACGGAAAAAATAATGGAGA	2888
Qy	2812	GACAAACGTCGAAAAACCTACAAATTTGGAAAAACAAACGAGTATATACAGAGGCGAAAAAGAGCT	2871
Db	2881	GACAAACGGGAAAAACCTACAAATTTGGAAAAACAAACGAGTATATACAGAGGCGAAAAAGAGCT	2940
Qy	2872	GTGGATGCTTTATTTTGTGTAGATTCTCAATATAATAGATTACAACGGGATACAAACATTTGGC	2931
Db	2941	GTGGATGCTTTATTTTGTGTAGATTCTCAATATGATCAATTACAACGGGATACAAACATTTGGC	3000
Qy	2932	ATGATTCAATCGGGCAGATAAAACCTTTGTTTCATCGAAATTCGAGAGGCTTATCTGTGAGAAATTA	2991
Db	3001	ATGATTCAATCGGGCAGATAAAACCTTTGTTTCATCGAAATTCGAGAGGCTTATCTTTTCAGAAATTA	3060
Qy	2992	TCTGTATCCCGGTGTAAATGTCGGAAAAATTTTGAAGAAATTAGAAGTCGCAATTATCACT	3051
Db	3061	CCTGTTATCCGAGTGTAAATGCGGAAAAATTTTGAAGAAATTAGAAGTCACATNTCACT	3120
Qy	3052	GCAATCTCCCTATACGATGCGAGAAATGTCTGTTAAAAATGGTGAATTTAATAATGGATTA	3111
Db	3121	GCAATGTCCTTATACGATGCGAGAAATGTCTGTTAAAAATGGTGAATTTAATAATGGATTA	3180
Qy	3112	GCATCTGGAAATGTAAAGGCGATGTAGATGTAACAACAGAGCCATCACCGTTCGTGCTT	3171
Db	3181	ACATGTTGGAAATGTAAAGGCGATGTAGATGTAACAACAGAGCCATCATCTGTCGACCTT	3240
Qy	3172	GTTATCCAGATGGGAAGCAGAAAGTGTCAACAGCAGTTCGCGTCTGTCCGGGGCGTGGC	3231
Db	3241	GTTATCCAGATGGGAAGCAGAAAGTGTCAACAGCAGTTCGCGTCTGTCCGGGGCGTGGC	3300
Qy	3232	TATATCTCTCGTGTCAAGCGTACAAGAGGGATATGGAGAGGGTGTGTAAACGATCCAT	3291
Db	3301	TATATCTCTCGTGTCAAGCGTACAAGAGGGATATGGAGAGGGTGTGTAAACGATCCAT	3360
Qy	3292	GAATTCAGAAACAAATACAGACGAACTTAATAATTTAAAAAATGTGAAGAGAGGAAGTGTAT	3351
Db	3361	GAATTCAGAAACAAATACAGACGAACTTAATAATTTAAAAAATGTGAAGAGAGGAAGTGTAT	3420
Qy	3352	CCACGGATACAGGAACGTCGTATGATTAATCTGCAACCAACGGTACAGCAGTATGTAAT	3411
Db	3421	CCACGGATACAGGAACGTCGTATGATTAATCTGCAACCAACGGTACAGCAGTATGTAAT	3480
Qy	3412	TCCCGTAAATGCTGGATATGAGGATGCAATATGAAGTTGATATAACAGCATCTGTGTAATTTAC	3471
Db	3481	TCCCGTAAATGCTGGATATGAGGATGCAATATGAAGTTGATATAACAGCATCTGTGTAATTTAC	3540
Qy	3472	AAACCGACTTATGAAGAAGAAAAAGTATACAGATGTACGAAGAGATAATCATTTGTGAATAT	3531
Db	3541	AAACCGACTTATGAAGAAGAAAAAGTATACAGATGTACGAAGAGATAATCATTTGTGAATAT	3600
Qy	3532	GACAGAGGTTATGTAATTAATCCACCACCTACAGCTGGTTATATGACAAAGAAATTTAGAA	3591
Db	3601	GACAGAGGTTATGTAATTAATCCACCACCTACAGCTGGTTATGTAACAAAGAAATTTAGAA	3660
Qy	3592	TACTTCCAGAAAAACCGATAAGGTATGGAATGGAATTTGGAAAAACGGAAAGGAAAGTTTAT	3651
Db	3661	TACTTCCAGAAAAACCGATAAGGTATGGAATGGAATTTGGAAAAACGGAAAGGAAAGTTTAT	3720
Qy	3652	GTAGACAGCGTGAATTTACTCTTATGGAGGAATAG	3687
Db	3721	GTAGATAGCGTGAATCTACTCTCTCATGGGAAGATAG	3756

RESULT 12
ADK98478
ID ADK98478 standard; DNA; 3687 BP.
XX
XX
AC ADK98478;
XX
DT 03-JUN-2004 (first entry)
XX
XX
DE B *thuringiensis* cry1Bb partial gene sequence SeqID1.
XX

insecticidal protein; plant; pesticide; gene therapy;
 lepidopteran insect pest; transgenic plant;
 insect infestation resistance; monocot; dicot; cry1Bb; gene; ds.
 Os
 Bacillus thuringiensis.

Key Location/Qualifiers
 CDS 1..3687
 /tag= a
 /product= "B thuringiensis cry1Bb"
 /partial
 /note= "No start or stop codon"

WO2004020636-A1.

11-MAR-2004.

26-AUG-2003; 2003WO-US026510.

29-AUG-2002; 2002US-0407428P.

(MONS) MONSANTO TECHNOLOGY LLC.
 (BOGD/) BOGDANOVA N N.
 (ROMA/) ROMANO C P.

Bogdanova NN, Romano CP;

WPI; 2004-269221/25.

P-PSDB; ADK98479.

New polynucleotide sequence optimized for expression of an insecticidal protein in a plant, useful in the control of Lepidoptera insect pests, and for producing transgenic plants with the ability to resist insect infestations.

Disclosure; SEQ ID NO 1; 138pp; English.

This invention relates to a novel polynucleotide sequence optimised for expression of an insecticidal protein in a plant. The invention may be useful for the production of pesticides whilst the disclosed sequences may be used for gene therapy. The polynucleotide sequence and methods are useful in the control of lepidopteran insect pests, and for producing transgenic plants with the ability to resist insect infestations. The invention provides polynucleotide sequences with enhanced, improved and optimised expression in monocot and dicot plant species. The present sequence is that of the (partial) B thuringiensis cry1Bb gene which is related to the invention.

Sequence 3687 BP; 1248 A; 621 C; 796 G; 1022 T; 0 U; 0 Other;

Query Match 72.8%; Score 2684.2; DB 12; Length 3687;
 Best Local Similarity 83.5%; Pred. No. 0;
 Matches 3085; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

1 TTGACTTCAAAATAGGAAAAATGAGAAATGAAATATATAATGCTTTATCGATTCCAGCTGTA 60
 1 TTGACTTCAATAGGAAAAATGAGAAATGAAATATATAATGCTTTATCGATTCCACGTA 60
 61 TCGAATCAATCCACAAATGGAATCTATCACAGATGCTCGTATTGAGGATCTTTTGT 120
 61 TCGAATCCTTCCACGAAATGAATCTATCACAGATGCTCGTATTGGAAGATAGCTTGT 120
 121 ATAGCCGAGGGGAATAATATCAATCCATCTGTAGCGCATCAAGTCCAAACGGGTATT 180
 121 GTAGCCGAGGTGAACAAATATTGATCCATTTGTAGCGCATCAAGTCCAAACGGGTATA 180
 181 AACATAGCTGGTAGAATACTAGTGTATTAGGCGTACCGTTTGTGGACAAATAGTAGT 240
 181 AACATAGCTGGTAGAATAATTGGGCGGTATTAGTGTGCCGTTTGTGGACAACTAGTAGT 240
 241 TTTTATAGTTTTCTTGTGGTGAATATTAGCCCGCGGCGAGAGATCAGTGGGAAATTTTC 300
 241 TTTTATAGTTTTCTTGTGGGGAATATTAGGCTAGTGGCAGAGATCCATGGGAAATTTTC 300

Qy 301 CTAGAACATGTCGAACAACTTTATAAATCAACAAATAACAGAAAAATGCTAGGAATACGGCA 360
 Db 301 CTGGAACATGTCGAACAACTTTATAAGACACAACTAACAGAAAAATCTAGGAATACGGCT 360
 Qy 361 CTTCCTCGATTACAAGGTTTAGGAGATTCCTTTAGAGCTTATCAACAGTCACTTGAAGAT 420
 Db 361 ATTGCTCGATTAGGAAGGCTTAGGAAGAGGCTTATAGATCTTTACCAGCAGGCTCTTTGAAACT 420
 Qy 421 TGGCTAGAAACCGTGTATGATGCAAGAACGAGAGAGTGTCTTTATACCAATATATATAGCC 480
 Db 421 TGGTTAGATACCCGAAATGATGCAAGATCAAGAAGCATTTCTTTGAGCGCTATGTTGCT 480
 Qy 481 TTAGAACTTGATTTTCTTAATGCCATGCGCTTTTTCGCAATTAGAAAAACAAAGAGTTCCA 540
 Db 481 TTAGAACTTGACATTACTCTGCTATACCGCTTTTTCAGAAATCGAAATGAAGAAGTTCCA 540
 Qy 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACCTTATTTATTATTGAGAGATGCTCT 600
 Db 541 TTAATTAATGGTATATGCTCAAGCTGCAAAATTTACCTTATTTATTATTGAGAGATGCTCT 600
 Qy 601 CTTTTCGTAGTGAATTTGGGCTTACATCGCAGGAAATTTCAACGTTATTATGAGCGCCAA 660
 Db 601 CTTTTCGTAGTGAATTTGGGCTTACATCGCAGGAAATTTCAACGTTATTATGAGCGCCAA 660
 Qy 661 GTGGAACAAACGAGAGATTTATTCGACTATTTCGCTAGATGCTATTAATACAGGTTCTAAAT 720
 Db 661 ATCAGATATACAGAGGAAATTTCTTAAACATTCGCTACATGCTATTAATACAGGTTCTAAAT 720
 Qy 721 AGCTTGAGAGGACAAATGCGCAAGTTGGGTGCTTATTAATCAATTCGCTAGAGATCTA 780
 Db 721 AACTTAAGAGGACAAATGCTGAAAGTTGGTGGGTATTAATCAATTCGCTAGAGATCTA 780
 Qy 781 ACCTTAGGGTATTAGATCTAGTGGCACTATTTCCCAAGCTATGACATCGCAGCTTATCCA 840
 Db 781 ACCTTAGGGTATTAGATTTAGTGGCTTATTTAGTAGCCCTATTCCCAAGCTATGATCTCGACCTTATCCA 840
 Qy 841 ATAAATACGAGTGTCTAGTTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGG 900
 Db 841 ATCAATACGAGTGTCTAGTTTAAACAGGGAAGTTTATACAGATCCAAATTTGGAGCAACAAAT 900
 Qy 901 GTAAAT-----ATGCGAAGTATGAATTTGGTATTAATTAATATGCACTTCGTTTCGGCT 954
 Db 901 GCACCTTCAGGATTTGCAAGTACGAAATTTGGTTTAAATAATATGCACTTCGTTTCGGCT 960
 Qy 955 ATAGAGACTGGTATTCGGAAGCGGCACTCTACTGATTTCTTCTAGACAACTTACAAAT 1014
 Db 961 ATAGAGCTGCCATTTTTCAGGCTTCGCACTCTACTGATTTTCCAGAACAACTTACAAAT 1020
 Qy 1015 TTTAGCACTTCATCAGATGGAGTGTACTAGGCGATATGACTTACTGGCGGGGACACACA 1074
 Db 1021 TACAGTGCATCAAGCGTTGGAGTACGCTCAACATATGAATTTATGGTGGGACATAGG 1080
 Qy 1075 ATCAATCTCGGCAATAGGAGCGGATTAATTAATCTCAACGCAATGG---GTCTACCAAT 1131
 Db 1081 CTTAACTTCGCGCCCAATAGGAGGACATTAATTAATCTCAACGCAATGGTTACTTAATAT 1140
 Qy 1132 ACTTCTATTAATCTCTGAAGATTAATCTTCTCTCGAGACGATTAATTTGAGACTGAATCA 1191
 Db 1141 ACTTCAATTAATCTCTGAACATTAACAGTTTACGCTCTCGAGACGTTTATGAGAACAGAAATCA 1200
 Qy 1192 TATCAGAGTGTCTCTATGGGGAATTTTACCTTGAACCTTATTCATGGTGTCCCTACTGTT 1251
 Db 1201 AATCAGGGAACAATAT-----ACTATTTACTCTCTGTGAATGGAGTACCTTTGGGCT 1254
 Qy 1252 AGATTTAATTTTAGAACCTCTCAGAACTCTTTTGAAGAGGATCTGCTAACTATAGTCAA 1311
 Db 1255 AGATTTAATTTTAAACCTCTCAGAAATTTTATGAAGAGCGCCACTACCTACAGTCAA 1314
 Qy 1312 CCCTATGAGTCACTGGGCTTCAATTAAGAAATTCAGAAATTCAGAAATTCACCAACGAAACA 1371
 Db 1315 CCGTATCAGGAGTTGGGATTTCAATTTATTTGATTCAGAAATTCAGAAATTCACCAACGAAACA 1374

QY	1372	ACGAAACGACAAATATAGATCATATAGTCATAGTTATCTCACATAGGCTCATTTCA	1431
Db	1375	ACGAAACGACAAATATAGATCATATAGTCATAGTTATCTCATATAGGCTCATTTCA	1434
QY	1432	CAATCTAGGGTGATGACAGATATATCTTGACGACCGTGTAGTCAGATCGTACAAAT	1491
Db	1435	GGAAACACTTTGAGAGCACCGATCTATCTTGGACGCATCGTAGTCAGATCGTACGAAT	1494
QY	1492	ACCATTAGTTACAGATAGCATAACAAATACATTTGGTAAATCATCTAACCTTAATCA	1551
Db	1495	ACGATTTGACCAATAGAAATACAAATACCAATTTGGTAAAGCAGCTGAATCTTTCAATCA	1554
QY	1552	GGTACCTCTGTAGTCAGTGCCCGAGATTTACAGGAGGGGATATAATCCGAACTAACGTT	1611
Db	1555	GGTTTACTTGTGTGGAGGCGCAGATTTACAGGTGGGATATCTTGTAGAACAAAT	1614
QY	1612	AATGGTAGTGACTAAAGTATGGGTCTTAATTTTAAATAATCATCTTACAGCGGTATCGC	1671
Db	1615	ACGGGTACATTTGGAGATATACGATTAATATTAATTAATTTTACAGGATATATCGC	1674
QY	1672	GTGAGAGTTCGTTATGCTGCTCTCAACAAATGGTCTGAGGGAATCTGTGCGAGGAGT	1731
Db	1675	GTAAAGATTCGTTATGCTCTACTACAGATTTTAAATTTTTCACGAGATTAATGGAACC	1734
QY	1732	ACTACTTTTTCATCAAGGATTCCTCTAGTACTATGAGTGCAAAATGAGTCTTTGACATCTCAA	1791
Db	1735	ACTGTTAATATGTTAAATTTCTCAAGAACTATGATAGGGGGATTAATTTAGATATAGA	1794
QY	1792	TCATTTAGATTTTCAGAAATTTCTGTAGTATGATCTGTCATCTGCGAGTCAAACTGCTGGA	1851
Db	1795	AGTTTTAGAACTCGAGATTTAGTACTCTCTTTTAAATTTTAAATGCCCACCAAGCACATTC	1854
QY	1852	ATAAGTATAGTAAATAGTCAGGTAGACAAACGTTTTCATTTGATAAATTTGATTT	1911
Db	1855	ACATTTGGGTCTCAGAGTTTTCAAATCAGGAAGTTTATATAGATAGCTCGAAATTTGTT	1914
QY	1912	CCAATTAATCTCAACCTTTGAAAGCAGAAATACGATTTAGAAAGGCGCAAGGCGGTGAAT	1971
Db	1915	CCAGCAGAGGTACATTTGAGGCGAGATATGATTTAGAAAGACACAAAGGCGGTGAAT	1974
QY	1972	GCTCTGTTTACTAATACGAATCCAAAGAAATGGAACAGATGTGACAGATATCATAT	2031
Db	1975	GCTCTGTTTACTTCTCAATCCAAAGAAATGGAACAGATGTGACAGATATCATAT	2034
QY	2032	GATCAAGATATCAATTTAGTGGCGTGTATTCGGATGAAATTCGTTAGATGAAAGAGN	2091
Db	2035	GACCAAGTGTCAATATAGTGGCGATTTATCAGATGAAATTTGCTTGGATGAAAGCGA	2094
QY	2092	GAAATTAATTTGAGAAAGTGAATATGCGAAACGACTCAGTGATGAAAGAACTTACTCCAA	2151
Db	2095	GAAATTAATTTGAGAAAGTGAATATGCGAAAGCAGTCTAGTGATGAAAGAACTTACTCCAA	2154
QY	2152	GATCCAAACTTACATCCATCAATAGCAACAGACTTCATATCTTACTAATAGCAATCG	2211
Db	2155	GATCCAAACTTACATCCATCAGTGGGCAATTAAGTTTCGATCCATCGATGCAATCA	2214
QY	2212	AATTTCCATCTATCATGAACAACTCTGAACATGGATGTGGGGAAGTGGAGACATTACA	2271
Db	2215	AATTTCCCTCTAATAGAGCTATCTGAACATGGATGTGGGGAAGTGGAGATGTTACC	2274
QY	2272	ATCCAGGAAGGAATGACGTATTTAAAGAGAAATTTACGTCACTACCGGGGACTTTTAAT	2331
Db	2275	ATTCAGGAAGGAATGACGTATTTAAAGAGAAATTTACGTCACTACCGGGTACTTTTAAT	2334
QY	2332	GAGTGTATCCGAGTATTTATATCAAAATAGGAGAGTTCGGAATTTAAAGCTTATATCT	2391
Db	2335	GAGTGTATCCAAATTTATATATCAAAATAGGAGAGTTCGGAATTTAAAGCTTATATACG	2394
QY	2392	CGCTACCAATTAAGAGGTATATTTGAAGATAGTCAAGATTTTAGAGATATATTTGATTCGT	2451
Db	2395	CGCTATCAATTAAGAGGTATATTTGAAGATAGTCAAGATTTTAGAGATATATTTAATTCGT	2454
QY	2452	TATAATGCGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGATATGGCGGCTTTCA	2511

Db	2455	TACATGCAAGCATGAACATTTGATGTTCCAGGTACCGATTCCTATGCGCGCTTTCA	2514
QY	2512	GTTGAAAGCCCAATCGGAAGGTGCGAGAAACCGAATCGATGCGCAACCAATTTTGAATGG	2571
Db	2515	GTTGAAAGCCCAATCGGAAGGTGCGAGAAACCGAATCGATGCGCAACCAATTTTGAATGG	2574
QY	2572	AATCTGATCTAGATTTGTTCTTCGAGAGATGAGAAATATGTCGCGATCATTTCCCATCAT	2631
Db	2575	AATCTGATCTAGATTTGTTCTTCGAGAGATGAGAAATATGTCGCGATCATTTCCCATCAT	2634
QY	2632	TTCTCTTTTGGATATGATATGATGTCAGACTTTCATGAGAATCTAGCGGTGCGGTG	2691
Db	2635	TTCACTTTTGGATATGATGTTGGGTGTCAGAGTTCATGAGAACCTAGCGGTGCGGTG	2694
QY	2692	GTATTCAGATTTAAGACGCAAGGTCTATGCAAGCTAGGGAATCTGGAATTTATTGAA	2751
Db	2695	GTATTCAGATTTAAGACGCAAGGTATGCAAGATTTAGGAATCTGGAATTTATTGAA	2754
QY	2752	GAGAAACCAATTTAGGAGAGCACTGTCTCTGTGTGAGAGAGCAGAGAAATATGAGA	2811
Db	2755	GAGAAACCAATTTAGGAGAGCACTGTCTCTGTGTGAGAGAGCAGAGAAATATGAGA	2814
QY	2812	GACAAACGTGAAATACTACAATTTGAAACAAACCGAGTATATACAGAGCAAAAGAGCT	2871
Db	2815	GACAAACGTGAAATACTACAATTTGAAACAAACCGAGTATATACAGAGCAAAAGAGCT	2874
QY	2872	GTGGATGCTTTTATTTGTAGATTTCTCAATATATAGATTAACAAGCGGATACAAACATTTGC	2931
Db	2875	GTGGATGCTTTTATTTGTAGATTTCTCAATATATGATCAATTTACAAGCGGATACAAACATTTGC	2934
QY	2932	ATGATTCATGCGGAGATAAATCTTCTCATCGAATTTGAGAGGCTTATCTGTGAGAAATTA	2991
Db	2935	ATGATTCATGCGGAGATAAATCTTGTTCATCGAATTTGAGAGGCTTATCTTTCAGAAATTA	2994
QY	2992	TCTGTTATCTCCGGGTGTAATCGGAAATTTTGAAGATTTAGAAGTTCGCAATTTATCACT	3051
Db	2995	CTGTTATCTCCAGGTGTAATCGGAAATTTTGAAGATTTAGAAGTTCACATTTATCACT	3054
QY	3052	GCAATCTCCTATACATGCGAGAAATGTCGTTTAAATATGATTTTAAATATGAGATTA	3111
Db	3055	GCAATGCTCCTATACATGCGAGAAATGTCGTTTAAATATGATTTTAAATATGAGATTA	3114
QY	3112	GCATGCTGGAATGTAAGGCGCATGTAGATGTACAACAGAGCCATCACCGTTCTGTCCCTT	3171
Db	3115	ACATGTTGGAATGTAAGGCGCATGTAGATGTACAACAGAGCCATCATCTGTCTGACCTT	3174
QY	3172	GTTATCCCAAGATGGAAGCAGAAAGTGTCAACAGCAGTTTCGCTGTGTCCGGGGCGTGGC	3231
Db	3175	GTTATCCCAAGATGGAAGCAGAAAGTGTCAACAGCAGTTTCGCTGTGTCCGGGGCGTGGC	3234
QY	3232	TATATCCTCCGTGTACAGCGTACAAGAGGATATGAGAGGTTGTGTACGATCCAT	3291
Db	3235	TATATCCTCCGTGTACAGCGTACAAGAGGATATGAGAGGTTGTGTACGATCCAT	3294
QY	3292	GAAATCGGAACAATACAGACGAACTTAAATTTTAAACCTGTGGAAGAGGAGTGTAT	3351
Db	3295	GAAATCGGAACAATACAGACGAACTTAAATTTTAAACCTGTGGAAGAGGAGTGTAT	3354
QY	3352	CCAACCGGATACAGGAACTGTATATCTGCAACCAAGGTAACAGCATGTGTAAT	3411
Db	3355	CCAACCGGATACAGGAACTGTATATCTGCAACCAAGGTAACAGCATGTGTAAT	3414
QY	3412	TCCCGTAACTGCTGGAATATGAGGATCGATATGAGTTGATCTACAGCATCTGTTAATAC	3471
Db	3415	TCCCGTAACTGCTGGAATATGAGGATCGATATGAGTTGATCTACAGCATCTGTTAATAC	3474
QY	3472	AAACCGACTTATGAAGAGAAACGATATACAGATGTACGAAGAGATAATCATTTGTGAATAT	3531
Db	3475	AAACCGACTTATGAAGAGAAACGATATACAGATGTACGAAGAGATAATCATTTGTGAATAT	3534
QY	3532	GACAGAGGATATGGAATTTATCCACCATACAGCTGGTTATATGACAAAAAGAAATTAAGAA	3591

Db 3535 GACAGAGGCTATGTGAATATTCCACAGTACCAGCTGGTTATGTGACAAAAGAAATTAGAA 3594
QY 3592 TACTTCCCAAGAACCGATAGCTGATTTGAGATTGGAGAAACGGAAGGGAAAGTTATT 3651
Db 3595 TACTTCCCAAGAACAGATACAGTATGGATTGGAGATTGGAGAAACGGAAGGGAAAGTTATT 3654
QY 3652 GTAGACAGCGTGAATTAATCTCTTATGGAGGAA 3684
Db 3655 GTAGATAGCGTGAATTAATCTCTCTATGGAGGAA 3687

RESULT 13

AAS04854
ID AAS04854 standard; DNA; 3627 BP.

AC AAS04854;

DT 07-SEP-2001 (first entry)

DE Bacillus thuringiensis DNA encoding partial mutant CryIbA.

KW Crystal protein; CryIIa; CryIbA; moth; butterfly; Colorado potato beetle;
KW ds; mutant.

OS Bacillus thuringiensis.

PH Key Location/Qualifiers
FT CDS 1..3627
FT /*tag= a
FT /product= "CryIbA"
FT /partial
FT /note= "No stop codon"
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..3651
FT /*tag= c
FT /label= Mature CryIbA
FT mutation replace(1464,A)
FT /*tag= d
FT mutation replace(1467,T)
FT /*tag= e

PN EP1099760-A1.

XX 16-MAY-2001.

XX 09-NOV-1999; 99EP-00203723.

XX 09-NOV-1999; 99EP-00203723.

XX (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.

XX De Maagd RA, Bosch HJ;

XX WPI; 2001-337141/36.

DR P-PSDB; AAU02094.

XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural
PT domains derived from at least 2 different crystal proteins, such as
PT CryIIa and CryIbA, and having insecticidal activity, useful for combating
PT insects.

XX Example; Page 22-23; 43pp; English.

XX The sequence encodes B. thuringiensis (Bt) crystal protein CryIbA,
CC mutated to allow cloning of domain III or domains I and II, to make the
CC hybrid protoxins of the invention. The hybrid toxins of the invention,
CC having structural domains I, II and III in this order starting from the N
CC -terminal derived from at least 2 different crystal proteins, are useful
CC for protecting plants against pest insects, e.g. moths, butterflies and
CC Colorado potato beetle or for combating insects

XX Sequence 3627 BP; 1184 A; 648 C; 820 G; 975 T; 0 U; 0 Other;

Db 947 CTGCGGCTATCCGGAAGCCCGCATCTACTTGTATTTCTAGAAACAACTTACAAATTTTAGCG 1006

Query Match

Beat Local Similarity 71.3%; Score 2630.2; DB 4; Length 3627;

Matches 3081; Conservative 0; Mismatches 533; Indels 81; Gaps 5;

QY 2 TGACTTCAAAATAGGAAAAATGAGAAATTAATAAATGCTTTATCGAATCCAGCTGTAT 61

Db 2 TGACTTCAAAATAGGAAAAATGAGAAATTAATAAATGCTTTATCGAATCCAGCTGTAT 46

QY 62 CGAATCATTTCCACACAAATGATCTATCACCAGATGCTCGTATTTCAGGATTTCTTTGTGA 121

Db 47 CGAATCATTTCCGACAAATGATCTATTTACCAGATGCTCGTATTTCAGGATTTCTTTGTGA 106

QY 122 TAGCCGAGGGAATAATATCAATCCACTTTGTAGGCAATCAACAGTCCAAACGGGTATTA 181

Db 107 TAGCCGAGGGAACAATATCGATCCATTTGTAGGCAATCAACAGTCCAAACGGGTATTA 166

QY 182 ACATAGCTGGTAGAATCTAGGTGTATTAGGGTACCGTTTGTCTGGACAAATAGTAGTT 241

Db 167 ACATAGCTGGTAGAATCTAGGCGGTATTGGGCGTACCGTTTGTCTGGACAACTAGCTAGTT 226

QY 242 TTTATAGTTTCTTGTGTCGAATTTATGGCCCGCGGCGAGAGATCAGTGGGAAATTTTCC 301

Db 227 TTTATAGTTTCTTGTGTCGAATTTATGGCCCGCGGCGAGAGATCAGTGGGAAATTTTCC 286

QY 302 TAGAACATGTCGAAACAACTTATAATCAACAAATAAGAAATGCTAGGAATACGGCAC 361

Db 287 TAGAACATGTCGAAACAACTTATAATCAACAAATAAGAAATGCTAGGAATACGGCTC 346

QY 362 TTGCTCGAATCAAGGTTTAGGAGATTCCTTTAGAGCTATCAACAGTCACTTTGAAGATT 421

Db 347 TTGCTCGAATCAAGGTTTAGGAGATTCCTTTAGAGCTATCAACAGTCACTTTGAAGATT 406

QY 422 GGCTAGAAAACCGTGATGATCGAAGACGAGAGTGTCTTTATACCCCAATATAGCCT 481

Db 407 GGCTAGAAAACCGTGATGATCGAAGACGAGAGTGTCTTTATACCCCAATATATAGCTT 466

QY 482 TAGAACTTGAATTTCTTAATCGGATGCGCTTTTCGCAATTTAGAAACCAAGAGTTCCAT 541

Db 467 TAGAACTTGAATTTCTTAATCGGATGCGCTTTTCGCAATTTAGAAACCAAGAGTTCCAT 526

QY 542 TATTAAATGGTATATGCTCAAGCTGCAATTTACACCTATTATTATTAGAGAGATGCTCTC 601

Db 527 TATTAAATGGTATATGCTCAAGCTGCAATTTACACCTATTATTATTAGAGAGATGCTCTC 586

QY 602 TTTTGGTGTAGTAATTTGGGCTTACATCGCAGGAAATTCACGTTATTATGAGCCCAAG 661

Db 587 TTTTGGTGTAGTAATTTGGGCTTACATCGCAGGAAATTCACGTTATTATGAGCCCAAG 646

QY 662 TGGAAACAAACGAGAGATTTATTCGCACTATTTCGCTAGAAATGCTATAATACAGTCTAAATA 721

Db 647 TGGAAACGACGAGAGATTTATTCGCACTATTTCGCTAGAAATGCTATAATACAGTCTAAATA 706

QY 722 GCTTGAGAGGACAAATGCGCAAGTTGGGTGCGTTTATAATCAATTCGCTAGAGATCTAA 781

Db 707 GCTTGAGAGGACAAATGCGCAAGTTGGGTGCGTTTATAATCAATTCGCTAGAGATCTAA 766

QY 782 CGTTAGGGTATTAGATCTAGTGGCACTATTTCGCAAGCTATGACACTCGCACTTATCCAA 841

Db 767 CGTTAGGGTATTAGATCTAGTGGCACTATTTCGCAAGCTATGACACTCGCACTTATCCAA 826

QY 842 TAAATACAGTGTCTCAGTTAAACAGGGAAGTTTATACAGAGCGCAATTCGAGCAACAGGGG 901

Db 827 TAAATACAGTGTCTCAGTTAAACAGGGAAGTTTATACAGAGCGCAATTCGAGCAACAGGGG 886

QY 902 TAAATATGGCAAGTATGAATTTGGTATTAATAATATGACCTTCGTTTCCGCTATAGAGA 961

Db 887 TAAATATGGCAAGTATGAATTTGGTATTAATAATATGACCTTCGTTTCCGCTATAGAGA 946

QY 962 CTGCGGTATCCGAAGCCCGCATCTACTTGTATTTCTAGAACAACTTACAAATTTTAGCA 1021

Db 947 CTGCGGTATCCGAAGCCCGCATCTACTTGTATTTCTAGAACAACTTACAAATTTTAGCG 1006


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Db 2630 CAGACTTAATAGGACTTAGTGTATGGTGTATTCAGATTAAAGACCAAGATGGCC 2689
QY 2720 ATGCAAGACTAGGAACTCGGAATTTATTGAAGAGAAACCAATTATTAGGAGAGCACTGT 2779
Db 2690 ATGCAAGACTAGGAACTTAGAGTTTCTGAAAGAGAAACCAATTATTAGGAGAGCACTAG 2749
QY 2780 CTCGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2839
Db 2750 CTCGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2809
QY 2840 CAAGAAGAGATATATACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2899
Db 2810 CAATATTTGTTTATAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2869
QY 2900 ATAATAGATTACAAGCGGATACAACATTTGGATGATTCATCGGAGAGATAAATTTGTT 2959
Db 2870 ATGATAGATTACAGTGGATACGACATCGCATGATTCATCGGAGAGATAAATCGGTT 2929
QY 2960 ATGGAATTCGAGAGGCTTATCTGTCAAGATTTATCTGTTATCCCGGTGTAAATGCGGAA 3019
Db 2930 ATAGAATCCGGAGAGCGTATCTGCCAGAGTTGTCTGTGATTCAGGTGTCAATGCGGCA 2989
QY 3020 TTTTGAAGAAATAGAGAGTTCGATATCATCTGCAATCTCCCTATACGATGCGAGAAATG 3079
Db 2990 TTTTGAAGAAATAGAGAGGACGTATTTTACAGCGGTATTTCTTATATATGATGCGAGAAATG 3049
QY 3080 TCGTTAAAAATGTTGATTTAATAATGAGATTAGCATGCTGGAATGTAAAGGCGCATGTAG 3139
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QY 3140 ATGTACAA---CAGAGCCATCACCGTTCTGTCTTCTGTTATCCAGAGAGAGAGAGAGAG 3196
Db 3110 ATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3169
QY 3197 TGTCAAGAGAGTTCGCTGCTGCGGCGGTGCTATATCTCCGTGTCAAGGCTACAG 3256
Db 3170 TGTCAAGAGAGTTCGCTGCTGCGGCGGTGCTATATCTCCGTGTCAAGGCTACAG 3229
QY 3257 AAGAGGATATGAGAGGCTGTGTAAAGATCCATGATGCTGGAATCCAGAGAGAGAGAGAG 3316
Db 3230 AAGAGGATATGAGAGGCTGCTGTAACGATCCATGATGCTGGAATCCAGAGAGAGAGAG 3289
QY 3317 TAAATTTTAAATCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3376
Db 3290 TGAATTTCAAGCAACTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3349
QY 3377 ATTATATGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3430
Db 3350 ATTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3409
QY 3431 AGGATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3490
Db 3410 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3469
QY 3491 AAACGTATATACAGATGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3550
Db 3470 AATCGTATATACAGATGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3529
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RESULT 15
AAS00421

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ID AC AAS00421;
XX 11-MAY-2001 (first entry)
DE B. thuringiensis Cry1Ba/Cry1Ca (BBC13) hybrid insecticidal toxin DNA.
KW Insecticidal agent; hybrid toxin; Cry1Ca; Cry1Ba; BBC13; insect control;
KW pest control; crop; insect resistant plant; transgenic plant;
KW crystal protein; mutant; ds.
XX Bacillus thuringiensis.
OS Synthetic.
XX Key Location/Qualifiers
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/partial
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/Note= "This sequence does not contain a stop codon"
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WO200114562-A1.

01-MAR-2001.

17-AUG-2000; 2000WO-EP008042.

19-AUG-1999; 99US-00377511.

(SYNG-) SYNGENTA PARTICIPATIONS AG.

De Maagd RA, Bosch HJ, Carozzi NB, Warren GW;

WPI; 2001-218452/22.

P-PSDB; AAU00420.

Novel hybrid insecticidal toxin useful for controlling insects such as Spodoptera exigua and Plutella xylostella, comprises domains I and II from CryIF or CryIB toxin joined to domain III from CryIC toxin.

Claim 6; Page 82-83; 99pp; English.

The present sequence encodes for 1 of 3 novel hybrid insecticidal toxins (AAU00419-AAU00422) and is designated BBC13. BBC13 comprises domains I and II from the CryIba toxin at the N-terminus joined to domain III from CryIca toxin at the C-terminus. In the 1186 amino acid PFC1 hybrid sequence, the junction between the CryIba and CryIca toxin domains corresponds to PFC1 residues 446-454. In the 1221 amino acid BBC13 and BBC15 hybrid sequences, the junction between the CryIba and CryIca toxin domains is residues 482-488 in the BBC13 hybrid, and residues 491-494 in the BBC15 hybrid. The hybrid toxins are constructed by cloning and in vivo recombination. The hybrid toxins are useful for controlling an insect such as Spodoptera exigua (beet armyworm), Manduca sexta (tobacco hornworm), Plutella xylostella (diamondback moth), Ostrinia nubilalis (European corn borer), Spodoptera frugiperda (fall armyworm), and Heliothis virescens (tobacco budworm) which are major causes of vegetable, fruit or ornamental flower crop losses. The nucleotide sequences encoding the hybrid toxins are useful for producing an insect-resistant plant by introducing the nucleotide sequence into the plant preferably a transgenic plant. The nucleotide sequences can also be expressed in microorganisms such as a virus, bacterium and fungus and the toxin produced used as an insecticidal agent. Baculoviruses engineered with the nucleotide sequence encoding a hybrid toxin can be used to infect insects in vivo resulting in their death. The hybrid toxins have a greater toxicity level than either of their parent toxins alone

Sequence 3663 BP; 1192 A; 651 C; 828 G; 992 T; 0 U; 0 Other;

Query Match 68.9%; Score 2541.2; DB 4; Length 3663;
Best Local Similarity 82.0%; Pred. No. 0;
Matches 3063; Conservative 0; Mismatches 548; Indels 123; Gaps 7;

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Job time : 1588 secs

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3260.2	88.4	3684	4	US-09-661-322A-62
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8	2687.2	72.9	3934	1	US-08-474-038-3
9	2687.2	72.9	3934	2	US-08-779-046-3
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12	1793.4	48.6	3522	1	US-08-291-368-1
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ALIGNMENTS

RESULT 1

US-09-661-322A-37

; Sequence 37, Application US/09661322A

; Patent No. 6593293

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Ruper, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos

; FILE REFERENCE: MECO201

; CURRENT APPLICATION NUMBER: US/09/661.322A

; CURRENT FILING DATE: 2000-09-13

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: Patent version 3.0

; SEQ ID NO 37

; LENGTH: 4173

; TYPE: DNA

; ORGANISM: Bacillus thuringiensis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3687)

US-09-661-322A-37

Query Match 99.4%; Score 3666.2; DB 4; Length 4173;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3674; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Db 2581 CTAGATTGTTCTCGCAGAGATGGAGAAAATGTGCGCATCATTCGCCATCATTTCTCTTTG 2640
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Db 2641 GATATTGATATTGGATGCACAGACTTGCATGAGAACTAGGCGTGGTGGTATTCAAG 2700
Qy 2701 ATTAAGCGCAGGAAGGTCATCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAACCA 2760
Db 2701 ATTAAGCGCAGGAAGGTCATCAAGACTAGGGAATCTGGAATTTATTGAAGAGAAACCA 2760
Qy 2761 TTATTAGGAAGCACTGCTCTGCTGTGAAGAGAGACAGAGAAAATATGGAGAGACAAACGT 2820
Db 2761 TTATTAGGAAGCACTGCTCTGCTGTGAAGAGAGACAGAGAAAATATGGAGAGACAAACGT 2820
Qy 2821 GAAAACTACAAATGGAAACAAAACGACTATATACAGAGGCAAAAGAAAGCTGTGGATGCT 2880
Db 2821 GAAAACTACAAATGGAAACAAAACGACTATATACAGAGGCAAAAGAAAGCTGTGGATGCT 2880
Qy 2881 TTATTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATGATTCAT 2940
Db 2881 TTATTGTAGATTCTCAATATAATAGATTACAAGCGGATACAAACATTTGGCATGATTCAT 2940
Qy 2941 GCGGAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTCAAGAAATATCTGTTATC 3000
Db 2941 GCGGAGATAAATCTGTTTCATCGAATTCGAGAGGCTTATCTGTCAAGAAATATCTGTTATC 3000
Qy 3001 CGGGGTGAATCGGGAATTTTCAAGAAATAGAGGTCGCATTCATCACTGCATCTCC 3060
Db 3001 CGGGGTGAATCGGGAATTTTCAAGAAATAGAGGTCGCATTCATCACTGCATCTCC 3060
Qy 3061 CTATACGATCGAGAAATGTCCTTAAAAATGGTGAATTTTAAATAGGATTAGCATGCTGG 3120
Db 3061 CTATACGATCGAGAAATGTCCTTAAAAATGGTGAATTTTAAATAGGATTAGCATGCTGG 3120
Qy 3121 AATGTAAAGGCGATGTAGATGTACACAGAGCCATCACCGTTCTGCTCTTCTGTTATCCCA 3180
Db 3121 AATGTAAAGGCGATGTAGATGTACACAGAGCCATCACCGTTCTGCTCTTCTGTTATCCCA 3180
Qy 3181 GAATGGGAGCAGAGTGTACACAGAGTTCGCTCTGTCGGGGCGGCTATATCTC 3240
Db 3181 GAATGGGAGCAGAGTGTACACAGAGTTCGCTCTGTCGGGGCGGCTATATCTC 3240
Qy 3241 CGTGTACAGCGTACAAAGAGGATATGAGAGGGTGTGTAAACGATCCATGAATCGAG 3300
Db 3241 CGTGTACAGCGTACAAAGAGGATATGAGAGGGTGTGTAAACGATCCATGAATCGAG 3300
Qy 3301 AACATACAGACGAATCTAAAAATTTTAAACCTGTGAAGAGAGGAAGTGTATCCACGGAT 3360
Db 3301 AACATACAGACGAATCTAAAAATTTTAAACCTGTGAAGAGAGGAAGTGTATCCACGGAT 3360
Qy 3361 ACAGGACGTGTAAATGATTACTTCCACAGGATACAGCAGTGTAAATCCGTTAT 3420
Db 3361 ACAGGACGTGTAAATGATTACTTCCACAGGATACAGCAGTGTAAATCCGTTAT 3420
Qy 3421 GCTGATATGAGATGCTATGAAAGTGTATCTACAGCATCTGTTAAATTAACAACCGACT 3480
Db 3421 GCTGATATGAGATGCTATGAAAGTGTATCTACAGCATCTGTTAAATTAACAACCGACT 3480
Qy 3481 TATGAAGAGAAACGTATACAGATGTACGAAGAGATAATCAATTTGTAATATGACAGAGG 3540
Db 3481 TATGAAGAGAAACGTATACAGATGTACGAAGAGATAATCAATTTGTAATATGACAGAGG 3540
Qy 3541 TATGTGAATTTATCCACCACTACCGATGTTATATGACAAAAGAAATTAAGAATCTTCCCA 3600
Db 3541 TATGTGAATTTATCCACCACTACCGATGTTATATGACAAAAGAAATTAAGAATCTTCCCA 3600

Qy 3601 GAAACCGATAGGTATGATTGAGATTGGAGAAACGGAAGGAAGCTTTATTGTAGACAGC 3660
Db 3601 GAAACCGATAGGTATGATTGAGATTGGAGAAACGGAAGGAAGCAATTCATCGTGACAGC 3660
Qy 3661 GTGGAATTAATCTCTTATGAGAGAAATAG 3687
Db 3661 ATAGAAATTAATCTCTTATGAGAAATAG 3687

RESULT 2

US-08-448-170-7
; Sequence 7, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: W/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-448-170-7

Query Match 88.6%; Score 3266.6; DB 1; Length 3684;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 3449; Conservative 0; Mismatches 229; Indels 15; Gaps 3;
Qy 1 TTGACTTCAATAGAAAATGAGAAATGAGAAATTAATAATGCTTTTATCGATTCAGCTCTGA 60
Db 1 TTGACTTCAATAGAAAATGAGAAATGAGAAATTAATAATGCTTTTATCGATTCAGCTCTGA 60
Qy 61 TCGAATCATTTCCACAAATGGATCTATCACCAGATGCTCGTATTTGAGGATTTCTTTGTGT 120

Db	1141	TCTATTAACTCTGTAAACATTTACAGTTCACATCTCGAGAGGTTTATAGAACAGAAATCATTT	1200
Qy	1195	GCAGGAGTCTTCTATGGGGAATTTACCTTGAACTTATCATGGTGCCCTACTGTTTGA	1254
Db	1201	GCAGGGAATAATAT-----ACTTCTAACTACTCTGTGAATGGAGTACCTTGGGCTAGA	1254
Qy	1255	TTTAAATTTTAGGAACCCCTCAGAATACTTTTGAAGAGGTACTGCTAACTATATAGTCAACCC	1314
Db	1255	TTTAAATGGAGAAATCCCTCGAATTCCTT---AGAGTAGCCTTCTCTATACTATAGG	1311
Qy	1315	TATGAGTCACTGGGCTTTCAAATTTAAAGATTTCAGAACTGAATACCAACAGAAACAACA	1374
Db	1312	TATCTGGAGTGGGACACAACTATTTGATTTCAGAACTGAATACCAACAGAAACAACA	1371
Qy	1375	GAAACACCAATATATGAATCATATAGTATAGTATAGTATCTCACATAGGCTCATTTCAACA	1434
Db	1372	GAAACACCAATATATGAATCTTACAGTCTATAGTATCTTAATATAGAACTATATACAGA	1431
Qy	1435	TCTAGGTTGCATGTATACAGTATATTTCTTGGACGCAACCGTAGTGCAGATCGTACAAATACC	1494
Db	1432	AACACTTTGAGAGCACCAAGTATATTTCTTGGACGCAACCGTAGTGCAGATCGTACAAATACC	1491
Qy	1495	ATTAGTTTCAGATAGCATAAACAAATACATTTGGTAAATCATTTCAAACCTTAATTCAGGT	1554
Db	1492	ATTAGTTTCAGATAGCATAAACAAATACCAATTTGGTAAATCATTTCAAACCTTAATTCAGGT	1551
Qy	1555	ACCTCTGTAGTCAGTGGGCCAGGATTTACAGAGGGGATATTAATCCGAACCTAACGTTAAT	1614
Db	1552	ACCTCTGTAGTCAGTGGGCCAGGATTTACAGAGGGGATATTAATCCGAACCTAACGTTAAT	1611
Qy	1615	GGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATTAATACAGCGGTATCGCGTG	1674
Db	1612	GGTAGTGTACTAAGTATGGGTCTTAATTTTAATAATACATTAATACAGCGGTATCGCGTG	1671
Qy	1675	AGAGTTCTGTATGCTGCTTCTCAAACATGCTCTGAGGTTAACTGTGCGAGGGAGTACT	1734
Db	1672	AGAGTTCTGTATGCTGCTTCTCAAACATGCTCTGAGGTTAACTGTGCGAGGGAGTACT	1731
Qy	1735	ACTTTTGATCAAGGATTCCTAGTACTATGAGTGCAATGAGTCTTTGACATCTCAATCA	1794
Db	1732	ACTTTTGATCAAGGATTCCTAGTACTATGAGTGCAATGAGTCTTTGACATCTCAATCA	1791
Qy	1795	TTTAGATTTGCAGAAATTTCTCTAGGTATAGTGATCTGGCAGTCAAACTGCTGGAATA	1854
Db	1792	TTTAGATTTGCAGAAATTTCTCTAGGTATAGTGATCTGGCAGTCAAACTGCTGGAATA	1851
Qy	1855	AGTATAGTAAATAGCAGGTAGACAAACGTTTCACTTTTGATAAAATTCGAATTCATTC	1914
Db	1852	AGTATAGTAAATAGCAGGTAGACAAACGTTTCACTTTTGATAAAATTCGAATTCATTC	1911
Qy	1915	ATTACTGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAGAGCGGTGAATGCT	1974
Db	1912	ATTACTGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGCGCAAGAGCGGTGAATGCT	1971
Qy	1975	CTGTTTACTAATACGAATCCAGAGAAATTTGAAAACAGATGTGACAGATTTATCATTTGAT	2034
Db	1972	CTGTTTACTAATACGAATCCAGAGAGTTTGAATAACAGGTGTGACAGATTTATCATTTGAT	2031
Qy	2035	CAAGTATCCAAATTTAGTGGCGTCTTTATCGGATGAATTTCTGCTTAGTAAAGAGAGAA	2094
Db	2032	GAAGTATCCAAATTTAGTGGCGTCTTTATCGGATGAATTTCTGCTTAGTAAAGAGAGAA	2091
Qy	2095	TTACTTGAGAAAGTGAATAATGCGAAACGACTCAGTGTGATGAAGAAAGAACTTACTCCAAGAT	2154
Db	2092	TTACTTGAGAAAGTGAATAATGCGAAACGACTCAGTGTGATGAAGAAAGAACTTACTCCAAGAT	2151
Qy	2155	CCAAACTTTCATCCATCAATAGCACCAAGTCTCATATCTACTATAGAGCAATCGAAT	2214
Db	2152	CCAAACTTTCATCCATCAATAGCACCAAGTCTCATATCTACTATAGAGCAATCGAAT	2211
Qy	2215	TTCACTATCCATGAAACATCTGAACATGGATGGTGGGGAAGTGAGAACATTTACAAATC	2274
Db	2212	TTCACTATCCATGAAACATCTGAACATGGATGGTGGGGAAGTGAGAACATTTACAAATC	2271

Db	61	TCGAATCATTTCCGCACAAATGAATCTATCAACCGATGCTCGTATTAGAGATAGCTTGTGT	120
Qy	121	ATAGCCGAGGGAATATATCAATCACTTGTAGCGCATCAACAGTCCAAACGGGTATT	180
Db	121	ATAGCCGAGGGAATATATCAATCACTTGTAGCGCATCAACAGTCCAAACGGGTATT	180
Qy	181	AACATAGCTGGTAGAATFACTAGGTGTATTAGGCGTACCCTTTGCTGGACAAATAGCTAGT	240
Db	181	AACATAGCTGGTAGAATFACTAGGTGTATTAGGCGTACCCTTTGCTGGACAAATAGCTAGT	240
Qy	241	TTTTATAGTTTCTTGTGTGTAATATAGCCCGCGCGCAGAGATCAGTGGGAAATTTTC	300
Db	241	TTTTATAGTTTCTTGTGTGTAATATAGCCCGCGCGCAGAGATCCTTTGGGAAATTTTC	300
Qy	301	CTAGACATCTCGAACCAACTTATAATCAACAATAACAGAAATGCTAGGAAATACGGCA	360
Db	301	CTAGACATCTCGAACCAACTTATAAGNCAACAAGTAAACAGAAATATCTAGGNTACGGCT	360
Qy	361	CTTGCTCGATTTACAAGGTTTAGGAGATTCCTTTTAGAGCCTATCAACAGTCACTTGAAGAT	420
Db	361	CTTGCTCGATTTACAAGGTTTAGGAGATTCCTTTTAGAGCCTATCAACAGTCACTTGAAGAT	420
Qy	421	TGGCTAGAAACCGTGATGATCAAGAACGAGAGTGTCTTTATACCCCAATATATAGCC	480
Db	421	TGGCTAGAAACCGTGATGATCAAGAACGAGAGTGTCTTTATACCCCAATATATAGCC	480
Qy	481	TTAGAACTTGATTTCTTAATGCGATCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA	540
Db	481	TTAGAACTTGATTTCTTAATGCGATCCGCTTTTCGCAATTAGAAACCAAGAAGTTCCA	540
Qy	541	TTATTAATAGTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGAGATGCTCT	600
Db	541	TTATTAATAGTATATGCTCAAGCTGCAAAATTTACACCTATTTATTTAGAGAGATGCTCT	600
Qy	601	CTTTTGGTAGTGAATTTGGGCTTACATCCAGAAATTCGCAATTTAGAAACCAAGAAGTTCCA	660
Db	601	CTTTTGGTAGTGAATTTGGGCTTACATCCAGAAATTCGCAATTTAGAAACCAAGAAGTTCCA	660
Qy	661	GTGAAACAAACGAGAGATTTTCGACTATTTGCGTAGAATGGTATAATACAGGTCTAAAT	720
Db	661	GTGAAACAAACGAGAGATTTTCGACTATTTGCGTAGAATGGTATAATACAGGTCTAAAT	720
Qy	721	AGCTTGAGAGGACAAATGCCGAAGTTGGTGGTATTAATCAATTCCTGAGAGATCTA	780
Db	721	AATTTGAGAGGACAAATGCCGAAGTTGGTGGTATTAATCAATTCCTGAGAGATCTA	780
Qy	781	ACGTTAGGGGTATTAGATCTAGTGCCACTATTCGCAAGCTATGACACTCGCACCTTATCCA	840
Db	781	ACGTTAGGGGTATTAGATCTAGTGCCACTATTCGCAAGCTATGACACTCGCACCTTATCCA	840
Qy	841	ATAAATACGAGTGTCTAGTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAGGG	900
Db	841	ATAAATACGAGTGTCTAGTTAAACAGGGAAGTTTATACAGACGCAATTTGGAGCAACAAAT	900
Qy	901	GTAAAT-----ATGCGCAAGTATGAATGGTGTATTAATATATGACCTTCGTTTTCGCT	954
Db	901	GTAAAT-----ATGCGCAAGTATGAATGGTGTATTAATATATGACCTTCGTTTTCGCT	954
Qy	955	ATAGAGACTGCGGTTTATCCGAGGCCGATCTACTTGAATTTTCTAGAACAACTTACAAAT	1014
Db	955	ATAGAGACTGCGGTTTATAGGCCCTCCGATCTACTTGAATTTTCCAGAACAGCTTACAAAT	1020
Qy	1015	TTTAGACTTCAATCAAGATGAGTGTACTAGGCAATGACTTACTGCGGGGGCACACA	1074
Db	1021	TTTAGACTTCAATCAAGATGAGTGTACTAGGCAATGACTTACTGCGGGGGCACACA	1080
Qy	1075	ATTTCAATCTCGGCAATAGGAGCGGATTAATATCTCAACGCTGGGTCTACCAATACT	1134
Db	1081	CTTGAATTCGCAACAAATAGGGGGTCAATTAAGTACTCTGACACACGGAATACCAATACT	1140
Qy	1135	TCTATTAAATCTGTGAAGATTAATCATTTCTCTCGAGACGTATATTTGAGCTGAATCATAT	1194

2275 CAGGAAGGAATGACGTATTTAAAGAGAAATTACGTACACTACCGGGACTTTTAAATGAG 2334
Db CAGGAAGGAATGACGTATTTAAAGAGAAATTACGTACACTACCGGGACTTTTAAATGAG 2331
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Db TGTATCCGACGTATTTATATCAAAAAATAGGGGAGCGGAAATTAAGAGCTTATATCTGC 2391
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Db TACCAATTAAGTGGCTATATTGAGATAGTCAAGATTTAGAGATATATTGATTCGTTAT 2451
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Db AATCGAAACATGAACATTGATGTTCCAGTACCGAGTCGATGCGCGCTTTCACTT 2511
2515 GAAAGCCCAATCGGAGGTGCGGAGAACCGAATCGATCGCACCACTTTTGAATGGAAT 2574
Db GAAAGCCCAATCGGAGGTGCGGAGAACCGAATCGATCGCACCACTTTTGAATGGAAT 2571
2575 CCTGATCTAGATGTTCTCGCAGAGATGGAGAAAAATGCGCATCATTTCCCATCATTTTC 2634
Db CCTGATCTAGATGTTCTCGCAGAGATGGAGAAAAATGCGCATCATTTCCCATCATTTTC 2631
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2695 TTCAAGATTAAGACGAGAGAGTCAAGCAAGTCTGGAATCTGGAATTTATGAAGAG 2754
Db TTCAAGATTAAGACGAGAGAGTCAAGCAAGTCTGGAATCTGGAATTTATGAAGAG 2751
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2815 AAACGTGAAAACTCAATTGGAACAAAAACAGGATATACAGAGGCAAAAGAGAGCTGT 2874
Db AAACGTGAAAACTCAATTGGAACAAAAACAGGATATACAGAGGCAAAAGAGAGCTGT 2871
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Db GATGCTTTATTTGATAGTCTCAATTAATAGATTAAGAGGATCAAAACATTTGGCATG 2931
2935 ATTCAATCGGAGATAACTGCTTCAATTCGAATTCGAGAGGCTTCTGTGCAATTTATCT 2994
Db ATTCAATCGGAGATAACTGCTTCAATTCGAATTCGAGAGGCTTCTGTGCAATTTATCT 2991
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3055 ATCTCCCTATAGATCGGAGAAATGTCGTTAAAAATGTTGATTTTAAATAGGATAGCA 3114
Db ATCTCCCTATAGATCGGAGAAATGTCGTTAAAAATGTTGATTTTAAATAGGATAGCA 3111
3115 TGCTGGAATGTAAGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 3174
Db TGCTGGAATGTAAGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 3171
3175 ATCCCAAGATGGAAGAGCAAGTGTCAAGAGGATTCGCGTCTGTCGCGGGGCGGCTAT 3234
Db ATCCCAAGATGGAAGAGCAAGTGTCAAGAGGATTCGCGTCTGTCGCGGGGCGGCTAT 3231
3235 ATCTCCCGTGTCAAGCGTACAAAGAGGATAGAGAGGGTGTGTAAACGATCCATGAA 3294
Db ATCTCCCGTGTCAAGCGTACAAAGAGGATAGAGAGGGTGTGTAAACGATCCATGAA 3291
3295 ATCGAGAACATACAGAGCACTAAATTTAAAACTGTGAAGAGAGGAGTGTATCCA 3354
Db ATCGAGAACATACAGAGCACTAAATTTAAAACTGTGAAGAGAGGAGTGTATCCA 3351

3355 ACGGATACAGGAACGTGTAATGATATATCTGACACCAAGGTAACAGCATGTATGTAATCC 3414
Db ACGGATACAGGAACGTGTAATGATATATCTGACACCAAGGTAACAGCATGTATGTAATCC 3411
3415 CGTAATGCTGATATGAGGATGCAATGAGTTGATCTACAGCATCTGTTTAAATACAAA 3474
Db CGTAATGCTGATATGAGGATGCAATGAGTTGATCTACAGCATCTGTTTAAATACAAA 3471
3475 CCGACTTATGAAGAGAAACGTATACAGATGTACGAAGAGATAATCATTTGTGAAATGAC 3534
Db CCGACTTATGAAGAGAAACGTATACAGATGTACGAAGAGATAATCATTTGTGAAATGAC 3531
3535 AGAGGATATGAAATTTATCCCACTACCACTGCTGTTATATGACAAAAAGAAATAGAAATAC 3594
Db AGAGGATATGAAATTTATCCCACTACCACTGCTGTTATATGACAAAAAGAAATAGAAATAC 3591
3595 TTCCAGAGAACCGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3654
Db TTCCAGAGAACCGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3651
3655 GACAGCGTGGAAATTAATCTCTTATGAGGAATAG 3687
Db GACAGCGTGGAAATTAATCTCTTATGAGGAATAG 3684

RESULT 3

US-08-961-803-5
; Sequence 5, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100

QY 1975 CTGTTTACTAATACGAATCCAAAGAGATTGAACACAGATGTGACAGATTTATCATATTGAT 2034
DB 1972 CTGTTTACTAAATACGAATCCAAAGAGATTGAACACAGATGTGACAGATTTATCATATTGAT 2031
QY 2035 CAAGTATCCAAATTTAGTGGCGTGTATTATCGGATGAATTTCTGCTTAGATGAAGAGAGAA 2094
DB 2032 GAAGTATCCAAATTTAGTGGCGTGTATTATCGGATGAATTTCTGCTTAGATGAAGAGAGAA 2091
QY 2095 TTACTTTGAGAAAGTGAATATATCGGAAACGACTCAGTGTATGAAGAAACCTTACTCCAAGAT 2154
DB 2092 TTACTTTGAGAAAGTGAATATATCGGAAACGACTCAGTGTATGAAGAAACCTTACTCCAAGAT 2151
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QY 2215 TTCACATCTATCCATGAACATCTGAACATGATGATGGGAGAGTGAAGAAACATTTACAATC 2274
DB 2212 TTCAATCTATCCATGAACATCTGAACATGATGATGGGAGAGTGAAGAAACATTTACAATC 2271
QY 2275 CAGGAAGGAAATGACGTATTTAAAGAGAAATACGTACACTACCGGGGACTTTTAAATGAG 2334
DB 2272 CAGGAAGGAAATGACGTATTTAAAGAGAAATACGTACACTACCGGGGACTTTTAAATGAG 2331
QY 2335 TGTATCCGACGTATTTATATCAAAAAATPAGAGAGTCGGAATTTAAAGCTTATATCTCGC 2394
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DB 2452 AATCGAAACATGAAACATTTGATGTTCCAGGTACCGAGTCGATGCGCGCTTCAGTT 2511
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DB 2512 GAAAGCCCAATCGGAAGTGGGAGAACCGAATCGATCGCACCACTTTTGAATGGAAT 2571
QY 2575 CCTGATCTAGATTTGTTCTTCAGAGATGAGAGAAATGTGGCATCATTTCCATCATTTTC 2634
DB 2572 CCTGATCTAGATTTGTTCTTCAGAGATGAGAGAAATGTGGCATCATTTCCATCATTTTC 2631
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DB 2692 TTCAAGATTAAAGACGAGGAAGGTCTATCAAGACTAGGGAATCTGGAAATTTATTGAAGAG 2751
QY 2755 AAACATTTATTAGGAGAGCATGTTCTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2814
DB 2752 AAACATTTATTAGGAGAGCATGTTCTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2811
QY 2815 AAACGTGAAACACTCAATTTGAAACAAAACGAGTATATACAGAGGCAAGAGAGAGAGAG 2874
DB 2812 AAACGTGAAACACTCAATTTGAAACAAAACGAGTATATACAGAGGCAAGAGAGAGAG 2871
QY 2875 GATGCTTTATTGTAGATTCTCAATATATATAGATTACAGCGGATACAAACATTTGGCATG 2934
DB 2872 GATGCTTTATTGTAGATTCTCAATATATATAGATTACAGCGGATACAAACATTTGGCATG 2931
QY 2935 ATTCAATCGGAGATAAACTTGTTCATCGAATTCGAGAGGCTTATCTGTGAGAAATTTATCT 2994
DB 2932 ATTCAATCGGAGATAAACTTGTTCATCGAATTCGAGAGGCTTATCTTTCAGAAATTTATCT 2991
QY 2995 GTTATCCCGGTGTAAATCGGAAATTTTGAAGAAATTTAGAGGTTCGCAATTTATCACTGCA 3054
DB 2992 GTTATCCCGGTGTAAATCGGAAATTTTGAAGAAATTTAGAGGTTCGCAATTTATCACTGCA 3051
QY 3055 ATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGTTGATTTTAAATGAGATTAGCA 3114

DB 3052 ATCTCCCTATACGATGCGAGAAATGTCGTTAAAAATGTTGATTTTAAATAATGATTAGCA 3111
QY 3115 TGCTGGAAATGAAAAAGGCGATGTAGATGTACACAGAGCCATCACCGTTCGTCTCTGTT 3174
DB 3112 TGCTGGAAATGAAAAAGGCGATGTAGATGTACACAGAGCCATCACCGTTCGTCTCTGTT 3171
QY 3175 ATCCAGAAATGCGGAAGCAGAAAGTGTCAACAGCAGTTCCGCTCTGTCCGGGGCGTGGCTAT 3234
DB 3172 ATCCAGAAATGCGGAAGCAGAAAGTGTCAACAGCAGTTCCGCTCTGTCCGGGGCGTGGCTAT 3231
QY 3235 ATCTCCGCTGTACAGCGGTACAAAAGAGGATATGAGAGGGTGTGTAAACGATCCATGAA 3294
DB 3232 ATCTCCGCTGTACAGCGGTACAAAAGAGGATATGAGAGGGTGTGTAAACGATCCATGAA 3291
QY 3295 ATCCAGAAATGCGGAAGCAGAACTAAAAATTTAAAAAATCTGTGAAGAGAGAGAGTGTATCCA 3354
DB 3292 ATCCAGAAATGCGGAAGCAGAACTAAAAATTTAAAAAATCTGTGAAGAGAGAGAGTGTATCCA 3351
QY 3355 ACAGATACAGGAACTGTAAATGATTATCTGCACACCAAGGTACAGAGTATGTAATTC 3414
DB 3352 ACAGATACAGGAACTGTAAATGATTATCTGCACACCAAGGTACAGAGTATGTAATTC 3411
QY 3415 CGTAAATGCTGATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3474
DB 3412 CGTAAATGCTGATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3471
QY 3475 CCGACTTATGAAGAGAAACGTATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3534
DB 3472 CCGACTTATGAAGAGAAACGTATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3531
QY 3535 AGAGGATATGAAATTTATCCACACTACCGCTGTTATATGACAAAAAGAAATAGAAATAC 3594
DB 3532 AGAGGATATGAAATTTATCCACAGTACCGCTGTTATATGACAAAAAGAAATAGAAATAC 3591
QY 3595 TTCCAGAAACCGATAAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3654
DB 3592 TTCCAGAAACCGATAAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3651
QY 3655 GACAGCTGGAAATTTACTCTTATCGAGGAATAG 3687
DB 3652 GACAGCTGGAAATTTACTCTTATCGAGGAATAG 3684

RESULT 4

US-09-661-322A-62

; Sequence 62, Application US/09661322A

; Patent No. 6593293

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Ruper, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos

; FILE REFERENCE: MISC0201

; CURRENT APPLICATION NUMBER: US/09/661,322A

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 62

; LENGTH: 3684

; TYPE: DNA

; ORGANISM: Bacillus thuringiensis

US-09-661-322A-62

Query Match 88.4%; Score 3260.2; DB 4; Length 3684;

Best Local Similarity 93.3%; Pred. No. 0;

Matches 3445; Conservative 0; Mismatches 233; Indels 15; Gaps 3;

QY 1 TTGACTTCAATAGGAAAAATGAGAAATTAATAATGCTTTTATCGAATCCAGCTGTA 60

Db 1 TTGACTTCAAAATAGGAAAAATGAGAAATGAAAATTATATAATGCTTTATTCGATTCACAGCTGTA 60
Qy 61 TCGAATCATTTCCACACAAATGGATCTATCAACAGATGCTCGTATTGAGGATTCCTTTGTGT 120
Db 61 TCGAATCATTTCCACACAAATGAAATCTATCAACGATGCTCGTATTGAGGATAGCTTTGTGT 120
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Db 121 ATAGCCGAGGGGAACAAATATCGATCCATTTGTTAGCGCATCAACAGTCCAAACGGGTATT 180
Qy 181 AACATAGCTGGTGAATATCTAGGTGTATTAGGGTACCGTTTCTGCTGGACAAATAGCTAGT 240
Db 181 AACATAGCTGGTGAATATCTAGGTGTATTAGGGTACCGTTTCTGCTGGACAAATAGCTAGT 240
Qy 241 TTTTATAGTTTCTTGTGTGGTAATATATGCCCCCGCGGAGAGATCACTGGGAAAAATTTTC 300
Db 241 TTTTATAGTTTCTTGTGTGGTAATATATGCCCCCGCGGAGAGATCCCTTGGGAAAAATTTTC 300
Qy 301 CTAGAACATGTCGAAACAACTTATTAATTAACAAATTAACAGAAATCTAGGAAATAGCGCA 360
Db 301 CTAGAACATGTCGAAACAACTTATTAATTAACAAATTAACAGAAATCTAGGAAATAGCGCT 360
Qy 361 CTGCTCGATTAACAGGTTTATAGAGATTCCTTTAGAGCCTTATCAACAGTCACTTTGAAGAT 420
Db 361 CTGCTCGATTAACAGGTTTATAGAGATTCCTTTAGAGCCTTATCAACAGTCACTTTGAAGAT 420
Qy 421 TGGCTAGAAAAACCGTGATGATGCAAGAAACGAGAAGTGTCTTTATATACCAATATATAGCC 480
Db 421 TGGCTAGAAAAACCGTGATGATGCAAGAAACGAGAAGTGTCTTTATATACCAATATATAGCC 480
Qy 481 TTAGAACTTGATTTCTTAATCGATGCCCTTTCCCAATTAGAAACCAAGAGTTTCCA 540
Db 481 TTAGAACTTGATTTCTTAATCGATGCCCTTTCCCAATTAGAAACCAAGAGTTTCCA 540
Qy 541 TTATTATGTTATATGCTCAAGCTGCAAAATTTACACCTATTAATTATGAGAGATGCTCT 600
Db 541 TTATTATGTTATATGCTCAAGCTGCAAAATTTACACCTATTAATTATGAGAGATGCTCT 600
Qy 601 CTTTTTGGTAGTAATTTGGCTTTACATCGCAGGAAATCAACGGTTTATATGAGCGCCAA 660
Db 601 CTTTTTGGTAGTAATTTGGCTTTACATCCCAAGAAATCAACGGTTTATATGAGCGCCAA 660
Qy 661 GTGAAACAAACGAGAGATTTCCGACTATTTGCGTAGAATGTTATATACAGTCTAAAT 720
Db 661 GTGAAACAAACGAGAGATTTCTGATTTATGCGCAAGATGTTATATACCGGTTTAAAT 720
Qy 721 AGCTTGAGAGGACAAATGCGCAAGTTGGGTGGCTTATATCAATTCAGTAGAGATCTA 780
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Qy 781 ACGTTAGGGGTATTAGATCTAGTGCGACTATTTCCCAAGCTATGACACTCGCACTTATCCA 840
Db 781 ACGCTAGGAGTATTAGATCTAGTGCGACTATTTCCCAAGCTATGACACGCGGTATTATCCA 840
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Db 841 ATGAATAACGCTGCTCAGTTAAACAGGGAAGTTTATACAGTATCCAAATTTGGAGAACAAAT 900
Qy 901 GTAAAT-----ATGCGCAAGTATGAATTTGGTATATATATATATGCACTCTGTTTTCCGCT 954
Db 901 GCACCTTCAGGATTTGCAAGTACGAATTTGGTTTATATATATATGCACTCTGTTTTCTGCC 960
Qy 955 ATAGAGACTGGGTTATCCGAAGCCGCACTCTACTTGTATTTCTAGAACACTTTACAAAT 1014
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Qy 1015 TTTTACACTTCATACAGTATGAGTCTAGGCAATATGACTTACTGCGGGGGGACACA 1074
Db 1021 TTTACGGTTATTAAGTCGATGGAGTAAATCTCAATATATGAATTAATCTAGGTTGGACATAGA 1080
Qy 1075 ATTTCAATCTCGCCCAATAGGAGCGGGAATTAATATCCTCAACGCAATGGGTCTACCAATCT 1134
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Db 1201 GCAGGGATAAATAT-----ACTTCTAACTACTCTCTGTAATGGAGTACCTTTGGGCTAGA 1254
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Db 1255 TTTTAAATGGAGAAATCCCTCGAAATTCCTTT---AGAGGTAGCCTTCTCTATACTATAGG 1311
Qy 1315 TATGAGTCACTCGGCTTCAATTAAGAACTTCAAGAACTGAATTTACACACAGAAACAAACA 1374
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Qy 1435 TCTAGGGTGCATGTACCGATATATTTCTGGACGCAACGCTAGTGCAGATCGTACAAATACC 1494
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Db 1492 ATTAGTTCAGATAGCATAAACAAATACCATTTGGTAAATCATTTCAACCTTTAAATTCAGGT 1551
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Db 1552 ACCTCTGATGTCAGTGGCCAGGATTTACAGAGGGGATATAAATCCGAACCTAACGTTAAT 1611
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Db 1612 GGTAGTGTACTTAAGTATGGGCTTAAATTTAATATAATCATATTAACGGGTATCGCGTG 1671
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Qy 1735 ACTTTTGTATCAAGGATTTCCCTAGTACTAGTGCAGAAATAGTCTTTGACATCTCAATCA 1794
Db 1732 ACTTTTGTATCAAGGATTTCCCTAGTACTAGTGCAGAAATAGTCTTTGACATCTCAATCA 1791
Qy 1795 TTTAGATTTGCAAGATTTTCCCTGATGTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1854
Db 1792 TTTAGATTTGCAAGATTTTCCCTGATGTTAGTGCATCTGGCAGTCAAACTGCTGGAATA 1851
Qy 1855 AGTATAAGTAATAATGCAAGTACAGAAACGTTTTCATTTGATATAAAATTTGAATTCATCCA 1914
Db 1852 AGTATAAGTAATAATGCAAGTACAGAAACGTTTTCATTTGATATAAAATTTGAATTCATCCA 1911
Qy 1915 ATTACTGCAACCTTTGCAAGCAGAAATACGATTTAGAAAGGCGCCAGAGCGGTGAATGCT 1974
Db 1912 ATTACTGCAACCTTTGCAAGCAGAAATACGATTTAGAAAGGCGCCAGAGCGGTGAATGCT 1971
Qy 1975 CTGTTTTACTAAATACGAATCCAAAGAGATTTGAAAAACAGATGTGACAGATTTATCATATTGAT 2034
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Qy 2035 CAAAGTATCCAAATTTAGTGGCGTTTATTCGGATGAATTTCTGCTTAGATGAAAGAGAGAA 2094
Db 2032 GAAAGTATCCAAATTTAGTGGCGTGTATTATCGGATGAATTTCTGCTTGGATGAAAGAGAGAA 2091
Qy 2095 TTTACTTGAAGAAAGTGAATATGCGAAACGACTCAGTGTGATGAAAGAACTTTACTCCAAGAT 2154
Db 2092 TTTACTTGAAGAAAGTGAATATGCGAAACGACTCAGTGTGATGAAAGAACTTTACTCCAAGAT 2151
Qy 2155 CCAAACTTCAATCCATCAATAAGCAACCAAGATCTTCAATCTCTATCTCTAATGAGCAATCGAAT 2214
Db 2152 CCAAACTTCAATCCATCAATAAGCAACCAAGATCTTCAATCTCTAATGAGCAATCGAAT 2211

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2212 TTCCATCTATCCATGAACAACTCTGAACATGGATGGTGGGAAAGTGAGAACATTCAATC 2271
2275 CAGGAAGGAATGACCTATTTAAAGAGAAATACGTCACACTACCGGGACCTTTAATGAG 2334
2272 CAGGAAGGAATGACCTATTTAAAGAGAAATACGTCACACTACCGGGACCTTTAATGAG 2331
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2515 GAAAGCCCAATCGGAAGGTGCGAGAAACCGAATCGATCGGCACACATTTTGAATGGAAT 2574
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2992 GTTATCCCGGCTGTAATTCGGAATTTTGAAGAAATTTAGAGGTCGATTTATCTGCA 3051
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3052 ATCTCCCTATACGATCGGAGAAATGCTGTTAAATGTTGATTTTAAATGGAATGATGCA 3111
3115 TGCTGGAATGTAAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3174
3112 TGCTGGAATGTAAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3171
3175 ATCCGAGAAATGGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3234
3172 ATCCGAGAAATGGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3231
3235 ATCTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3294
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3295 ATCGAGAAACATACAGAGAACTAAAAATTTAAAAATCTGTGAAGAGAGAGAGAGATGATCCA 3354

3292 ATCGAGAAACATACAGAGAACTAAAAATTTAAAAATCTGTGAAGAGAGAGAGATGATCCA 3351
3355 ACGGATACAGAGAACTGTAAATGATTTACTGACACCAAGGTACAGCAGTATGTAATGCC 3414
3352 ACGGATACAGAGAACTGTAAATGATTTACTGACACCAAGGTACAGCAGTATGTAATGCC 3411
3415 CGTAATGCTGGATATGAGAGTGCATATGAAGTTGATCTACAGCATCTGTTAATTAACAAA 3474
3412 CGTAATGCTGGATATGAGAGTGCATATGAAGTTGATCTACAGCATCTGTTAATTAACAAA 3471
3475 CCGACTTATGAAGAGAAACCGTATACAGATGTACGAAGAGATTAATCATTTGTGAATATGAC 3534
3472 CCGACTTATGAAGAGAAACCGTATACAGATGTACGAAGAGATTAATCATTTGTGAATATGAC 3531
3535 AGAGGGTATGTAATTTATCCACCTACAGCTGGTATATGACAAAAGAAATAGAAATAC 3594
3532 AGAGGGTATGTAATTTATCCACCTACAGCTGGTATATGACAAAAGAAATAGAAATAC 3591
3595 TTCCAGAGAAACCGATTAAGGTATGAGATTGAGAAACCGAAAGGAGAGTTTATTGTA 3654
3592 TTCCAGAGAAACCGATTAAGGTATGAGATTGAGAAACCGAAAGGAGAGTTTATTGTA 3651
3655 GACAGCGTGGAAATTAATCTCTTATGGAGGAATAG 3687
3652 GACAGCGTGGAAATTAATCTCTTATGGAGGAATAG 3684

RESULT 5

US-08-377-690-1
; Sequence 1, Application US/08377690
; Patent No. 5628995
; GENERAL INFORMATION:
; APPLICANT: PEPEROEN, Marnix
; APPLICANT: JANSSENS, Stefan
; APPLICANT: DENOLF, Peter
; TITLE OF INVENTION: CONTROL OF OSTRINIA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: The George Mason Bldg., Washington & Prince
; STREET: S.E.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,690
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,781
; FILING DATE:
; APPLICATION NUMBER: US 07/938,362
; FILING DATE: 31-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feuty, Sharon B
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-039
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

```
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: entomocidus HD 110
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 186..3872
; OTHER INFORMATION: /note= "PROPERTIES: CryIB is toxic to
; OTHER INFORMATION: Ostrinea nubilalis (among others)"
; US-08-377-690-1

Query Match      85.0%; Score 3133.6; DB 1; Length 4074;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 3373; Conservative 0; Mismatches 299; Indels 30; Gaps 3;

Qy 1 TTGACTTCAAAATAGGAAAAATGAGAAATTAATAATGCTTTATCGATTCGAGCTGTA 60
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Db 291 ATAGCCGAGGGGAATTAATGATCCATTGTTGTAGGCGCATCAACAGTCCAAACGGGTATT 350
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Qy 301 CTAGAAATCTCGAAACAACTTATAAATCAACAAATAGCAAAATGCTAGGAATACGGCA 360
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Db 531 CTTGCTCGATTACAGGTTAGGAGATTCCTTTAGAGCTCATCAACAGTCACTTGAAGAT 590
Qy 421 TGCTAGAAACCGTGATGATCAAGAACGAGAGTGTCTTTATACCCCAATATATAGCC 480
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Db 711 TTATTAAATGATATATGCTCAAGCTGCAAAATTTACCTATTATTATGAGAGATGCTCT 770
Qy 601 CTTTGTGGTAGTGAATTTGGGCTTACATCCGAGAAATTCAGGTTATTATGAGCGCCAA 660
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Qy 661 GTGGAAACAAACGAGAGATTTATCCGATTTGGTGAAGATGCTATATACAGGCTCTAAAT 720
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Db 951 ACGTTAGGGGTATTAGATCTAGTGGCACTATTCACAGCTATGACACTCCGACTTATCCA 1010
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Qy 961 GTAAATATGGCAAGTATGAATTTGGTATTAATAATGCAACCTTCTGCTCATAGAG 1130
Db 1071 GTAAATATGGCAAGTATGAATTTGGTATTAATAATGCAACCTTCTGCTCATAGAG 1190
Qy 961 ACTGGGGTTATCCGAAGCCCGCATCTACTTGAATTTCTAGAGCAACCTTACAATTTTAGC 1020
Db 1131 GCTGGGGTTATCCGAAGCCCGCATCTACTTGAATTTCTAGAGCAACCTTACAATTTTAGC 1190
Qy 1021 ACTTCATACGATGAGTGTCTACTAGGCAATGACTTACTGGGGGGGACACAATTCAA 1080
Db 1191 GCTTCATACGATGAGTGTCTACTAGGCAATGACTTACTTATGGGGGGGACACGATTCAA 1250
Qy 1081 TCTCGGCCAATAGGAGGCGGATTAATACCTCAACGCGATGGGTCTACCAATCTCTATT 1140
Db 1251 TCTCGGCCAATAGGAGGCGGATTAATACCTCAACGCGATGGGTCTACCAATCTCTATT 1310
Qy 1141 AATCCTGTGAAGATTTATCATTTCTCTCGAGACGTATATTGGACTGAATCATATGCAGGA 1200
Db 1311 AATCCTGTGAAGATTTATCATTTCTCTCGAGACGTATATTGGACTGAATCATATGCAGGA 1370
Qy 1201 GTGCTTCTATGGGAAATTTACCTTGAA CCTATTCTATGCTGCTCCCTACTGTTAGATTTAAT 1260
Db 1371 GTGCTTCTATGGGAAATTTACCTTGAA CCTATTCTATGCTGCTCCCTACTGTTAGATTTAAT 1430
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Db 1431 TTTAGGAAACCTTCAGAAATCTTTTGAAGAGGTACTGCTAACTATATAGTCAACCTATAG 1490
Qy 1321 TCACCTGGGCTTCAATTAAGAAATTCAGAAAACTGAATTACCACCAAGAAACAAACAGAACGA 1380
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Qy 1381 CCAAAATATGAATTCATATAGTCAATAGTTATCTCACAATAGGGCTCAATCAATCTAG 1440
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Qy 1561 GTAGTCAGTGGCCAGGATTTACAGAGGGGATATTAATCCGAACTAACGGTTAATGGTAGT 1620
Db 1731 GTTGTAGAGGACAGGATTTACTGTTGGGGATATTCTTCGAAGAACGAATACTGTTGGA 1790
Qy 1621 GTACTAAGTATGGGTCTTAATTTTAATAATACATCATTACAGCGGTATCGCGTGAAGTT 1680
Db 1791 TTTGGAACGATAGAGTAACTGTTAACGGACCAATTAACCAAGATATCGTATAGGATTC 1850
Qy 1681 CGTTATGCTGCTTCTCAAAACATGGTCTCGAGGGTAACTGTTCGGAGGGAGTACTACTTTT 1740
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RESULT 6

US-08-100-709-3

; Sequence 3, Application US/08100709

; Patent No. 5322687

; GENERAL INFORMATION:

; APPLICANT: Donovan, William P.

; APPLICANT: Tan, Yuping

; APPLICANT: Jany, Christine S.

; APPLICANT: Gonzalez Jr., Jose M.

; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5

; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

; ADDRESSEE: Nadel

; STREET: 1601 Market Street, 36th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/100.709

; FILING DATE: 19930729

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 67..3756
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2253..2272
US-08-100-709-3

Query Match 72.98; Score 2687.2; DB 1; Length 3934;
Best Local Similarity 83.54; Pred. No. 0;
Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

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3541 AAACCGACTTATGAAGAAACGCTATACAGATGTACAGAGATTAATCATTTGGAATAT 3600
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3592 TACTTCCAGAAACCGATTAAGGTATGGAATGAGATTTGAGAAACCGAAAGGAGTTTATT 3651
3661 TACTTCCAGAAACCGATTAAGGTATGGAATTTGAGATTTGAGAAACCGAAAGGAGTTTATT 3720
3652 GTAGACAGCTGGAAATTAATCTCTTATGGAGAAATAG 3687
3721 GTAGATAGCTGGAAATTAATCTCTTATGGAGAAATAG 3756

RESULT 7

US-08-176-865-3

; Sequence 3, Application US/08176865

; Patent No. 5616319

; GENERAL INFORMATION:

; APPLICANT: Donovan, William P.

; APPLICANT: Tan, Yiping

; APPLICANT: Jany, Christine S.

; APPLICANT: Gonzalez Jr., Jose M.

; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYST4 AND CRYST5

; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

; ADDRESSEE: Nadel

; STREET: 1601 Market Street, 36th Floor

; CITY: Philadelphia

STATE: Pennsylvania		Db		547	TTAGAACTTGACATTA	606
COUNTRY: U.S.A.		Qy		541	TTATTAATGTTATATGCTCAAGCTGCAAAATTTACACTATTTATTTATTTAGAGAGATGCTCT	600
COMPUTER: IBM PC compatible		Db		607	TTATTAATGTTATATGCTCAAGCTGCAAAATTTACACTATTTATTTATTTAGAGAGATGCTCT	666
OPERATING SYSTEM: PC-DOS/MS-DOS		Qy		601	CTTTTGGTGTAGTAAATTTGGGCTTACATCGCAGGAAATTCACAGTTATTTATGAGCGCAA	660
SOFTWARE: PatentIn Release #1.0, Version #1.25		Db		667	CTTTTGGTGTAGTAAATTTGGGCTTACATCGCAGGAAATTCACAGTTATTTATGAGCGCAA	726
CURRENT APPLICATION DATA:		Qy		661	GTGGAACAAACGAGAGATTTATCCGACTATTTGGGTGAGAAATGGTATATATACAGGCTTAAAT	720
APPLICATION NUMBER: US/08/176,865		Db		727	ATCAGATATACAGAGGAAATTTCTAACAATGGTACAAATGGTATATATACAGGCTTAAAT	786
CLASSIFICATION: 435		Qy		721	AGCTTGAGAGGGAACAAATGCGGCAAGTTGGGTGGGTTATTAATCAATTTCCGTAGAGATCTA	780
PRIOR APPLICATION DATA:		Db		787	AACTTAAGAGGGAACAAATGCTGAAAGTTGGTGGGTTATTAATCAATTTCCGTAGAGATCTA	846
APPLICATION NUMBER: US 08/100,709		Qy		781	ACGTTAGGGTATTTAGATCTAGTGGCACTATTTCCCAAGCTATGACACTCGCCTTATCCA	840
FILING DATE: 29-JUL-1993		Db		847	ACGTTAGGGTATTTAGATCTAGTGGCACTATTTCCCAAGCTATGACACTCGCCTTATCCA	906
ATTORNEY/AGENT INFORMATION:		Qy		841	ATAAATACGAGTCTCAAGTTAAACAGGGAAGTTTATACAGCGCAATTTGAGCGAACAGGG	900
NAME: Egolf, Christopher		Db		907	ATCAATACGAGTCTCAAGTTAAACAGGGAAGTTTATACAGATCCCAATTTGGGAGAACAAAT	966
REGISTRATION NUMBER: 27633		Qy		901	GTAAAT-----ATGGCAAGTATGAAATTTGGTATTAATTAATTAATTAATTAATTAATTAAT	954
REFERENCE/DOCKET NUMBER: 7205-49		Db		967	GCACCTTCAGGATTTGCAAGTACGAATTTGGTATTAATTAATTAATTAATTAATTAATTAAT	1026
TELECOMMUNICATION INFORMATION:		Qy		955	ATAGAGACTGCGGTTATCCGGAAGCCCGCATCTACTTTGATTTTATGAAACAACTTACAAAT	1014
INFORMATION FOR SEQ ID NO: 3:		Db		1027	ATAGAGGCTGCCATTTTCAGGCCCTCCGCACTCTACTTTGATTTTTCAGAAACAACTTACAAAT	1086
SEQUENCE CHARACTERISTICS:		Qy		1015	TTTAGACATTTATCAACGATGAGTGTCTACTAGGCAATATGACTTACTGCGGGGCGACACA	1074
LENGTH: 3934 base pairs		Db		1087	TACAGTGCAATCAAGCCGTTGGAGTAGCACTCAACATATGAAATTTATGGGTGGGACATAGG	1146
TYPE: nucleic acid		Qy		1075	ATTCATATCTCGCCCAATAGGAGCGGATTTAAATACCTCAAGCGCATGGGTCTACCA---AT	1131
STRANDEDNESS: double		Db		1147	CTTAACTTCGCGCCCAATAGGAGGGAATTAATACCTCAACACAAAGGACTTACTAATAAT	1206
TOPOLOGY: circular		Qy		1132	ACTTCTTATTAATCCGTGAAGATTTATCACTTCTCTCGAGAGCTATATTTGGACTGAATCA	1191
MOLECULE TYPE: DNA (genomic)		Db		1207	ACTTCAATTTAACTCTGTAACATTTACAGTTTACGTTCTCGAGAGCTTTTATAGAAACAAATCA	1266
FEATURE:		Qy		1192	TATGAGAGGAGTGTCTCTATGCGGAAATTTACCTTGAACCTTATTCATGGGTGCTCCTACTGTT	1251
NAME/KEY: CDS		Db		1267	AATGCGAGGGAACAAATAT-----ACTATTTACTCTCTCTGTAATGGAGTACCTTTGGGCT	1320
LOCATION: 67..3756		Qy		1252	AGATTTTAAATTTTAGGAAACCTCAGAAATCTTTTGAAGAGGTAAGTCTAACTATAGTCAA	1311
FEATURE:		Db		1321	AGATTTTAAATTTTATAAACCTCAGAAATATTTATGAAGAGGCGCCACTACCTACAGTCAA	1380
LOCATION: 2253..2272		Qy		1312	CCCTATGAGTCACTGGCTTCGATTTAAAGATTTCAAGAACTGAATTTACCAACAGAAACA	1371
US-08-176-865-3		Db		1381	CCGTATCAGGAGTGGGATTTCAATTTATTTGATTTAGAAACCTGAATTTACCAACAGAAACA	1440
Query Match		Qy		1372	ACAGAACGACCAAAATTTATGAATCATATAGTCTATAGGTTATCTCAATAGGGCTCATTTCA	1431
Best Local Similarity 83.5%; Pred. No. 0;		Db		1441	ACAGAACGACCAAAATTTATGAATCATATAGTCTATAGGTTATCTCAATAGGACTAATCATA	1500
Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;		Qy		1432	CAATCTAGGTGCAATGTAACAGTATATTTCTTGAACGCAACCGTAGTGCAGATCCGTACAAAT	1491
1 TTGACTTCAATAGGAAAAATGAGAAATGAAATTTAAATGCTTTTATCGATTTCCAGCTGTA		Db		1501	GGAAACACTTTTGAGAGCAACAGTCTATTTCTTGGACGCACTGATGCGAGATCGTACGAAT	1560
67 TTGACTTCAATAGGAAAAATGAGAAATGAAATTTAAATGCTTTTATCGATTTCCAAACGGTA		Qy		1492	ACCAATTTAGTTGAGATGACATAACCAAAATACCAATTTGGTAAATCATTTCAACCTTAAATCA	1551
61 TCGAATCATTTCCACA CAATGATCTATCAACAGATGCTCGTATGAGGATCTTCTGT		Db		1561	ACGATTTGGAACAAATAGAAATTAACAAATACCAATTTGGTAAAGCACTGAATCTTCTATTCA	1620
127 TCGAATCCTTCCACGCAATGAATCTATCACCAGATGCTCGTATTTGAAGATAGCTTGT		Qy		1552	GGTACCTCTGTAGTCACTGGCCGAGGATTTACAGGAGGATTTATCCGAACTTAACTTCA	1611

Db 1621 GGTGTTACTGTTGTTGGAGGGCCAGATTTACAGTGGGGATATCCTTCGTAGACAAAT 1680
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Db 1681 ACGGCTACATTTGGAGATATACGATTAATTAATGTGCCATTTATCCAAAGATATCGC 1740
Qy 1672 GTGAGATTGTTATGCTGCTCTCAACAATAGTCTTGAAGGTTAACTGTCCGAGGGAGT 1731
Db 1741 GTAAGGATTCGTTATGCTCTTACTACAGATTTACAAATTTTTCACGAGAAATTAATGGAACC 1800
Qy 1732 ACTACTTTTATCAAGGATTCCTAGTACTATGATGCAATAGATCTTTGACATCTCAA 1791
Db 1801 ACTGTTAATATTTGGTAAATTTCTCAAGAACTATGAATAGGGGGGAAATTTTGAATATAGA 1860
Qy 1792 TCATTTAGATTTGCAGAAATTTCTGTAGTATTTAGTGCATCTGGCAGTCAAACTGCTGGA 1851
Db 1861 AGTTTGAAGCTGAGGATTTAGTACTCTTTTAAATTTTAAATGCCCAGCAATTC 1920
Qy 1852 ATAAGTATAAGTAAATGCAAGTTAGACAAAGCTTTTCACTTTGATPAAATTTGAATTCAT 1911
Db 1921 ACATTTGGGTGCTCAGAGTTTTCAAATCAGGAAGTTTATATAGATAGAGTCCGAATTTGTT 1980
Qy 1912 CCNATTACTGCNACTTCGAGCAGAAATACGATTTAGAAAGGGCCAGAGCGGTGAAT 1971
Db 1981 CCAGCAGAGGTAACATTTGAGCAGAAATATGATTTAGAAAGAGCACAAAAGGCGGTGAAT 2040
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Db 2041 GCTCTGTTTACTTCTACAAATCCAAAGAGATTTGAAACAGATGTGACAGATTTATCATATT 2100
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Qy 2092 GAATTTACTTGGAGAGTGAATATCGGAAACGACTCAGTGTATGAAAGAACTTACTCCAA 2151
Db 2161 GAAATTTTGAAGAGTGAATATCGGAGCGACTCAGTGTATGAAAGAACTTACTCCAA 2220
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Db 3661 TACTTCCAGAAACCGATTAAGTATGATTTGAGATTTGAGAGAAACGAGAGGAAATTTATT 3720
Qy 3652 GTAGACAGCGTGGAAATTTACTCTTTATCGAGGAATAG 3687
Db 3721 GTAGATAGCGTGGAACTACTCTCTCATCGAAGAAATAG 3756

RESULT 8
US-08-474-038-3
; Sequence 3, Application US/08474038

Db 1381 CCGTATCAGGAGTGGGATTCAATTAATTTGATTTCAGAAATGAATATCCACAGAAACA 1440
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Qy 1492 ACCATTAAGTTCAGATAGCATATAACAAATACCAATGGTAAATCATTTCAACCTTAATTTCA 1551
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Qy 1552 GGTACTCTGTAGTCAAGTGGCCAGGATTTACAGGAGGGGATATTAATCCGAACTAAAGCTT 1611
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Db 2041 GCTCTGTTTACTTCTACAAATCCAAAGAGATTTGAAACAGATGTGACAGATTAATCATATT 2100
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1372 ACAGAACGACCAAAATATGAATCATATAGTATAGTCTATCTCATAGGCTCATTTCA 1431
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1741 GTAAGGATTCGTATGCTTCTACTACAGATTTACAAATTTTTCACAGAAATTAATGGAACC 1800
1732 ACTACTTTGTGATCAAGGATTCCTAGTACTATAGTGCAAATAGTCTTTGACATCTCAA 1791
1801 ACTGTTAATAATGGTAAATTTCTCAAGAACTATGAATAGGGGGATTAATTTAGAAATATAGA 1860
1792 TCATTTAGATTTGCAGAAATTTCTCTAGGTATTTAGTGCATCTGGCAGTCAAACTGCTGGA 1851
1861 AGTTTGAAGCTGAGGATTTAGTACTCTCTTTAATTTTAAATGCCCAGCAATTC 1920
1852 ATAAGTATAAGTAAATATGACAGGTAGACAAACGTTTCTACTTTGATPAATAATTCATTT 1911
1921 ACATTTGGGTCTCAGAGTTTTTCAAAATCAGGAAGTTTATATAGATAGAGTCGAATTTGTT 1980
1912 CCNATTTAGTCAACCTTCGAGAGCAAAATACGATTTAGAAAGGGCCAGAGCGGTGAAT 1971
1981 CCAGCAGAGGTAACTATTTGAGGAGCAAAATATGATTTAGAAAGAGCAAAAGGCGGTGAAT 2040
1972 GCTCTGTTTAAATACCAATCCAAAGAGATTGAAACAGATGTGACAGATTTATCATATT 2031
2041 GCTCTGTTTACTTCTACAAATCCAAAGAGATTGAAACAGATGTGACAGATTTATCATATT 2100
2032 GATCAAGTATCCAAATTTAGTGGGTTTATCGGATGAATTTCTGCTAGATGAAAGAGA 2091
2101 GACCAAGTGTCCAAATGATGGCATGTTTATCAGATGAATTTTGTCTGGATGAGAAGCGA 2160
2092 GAAATTTCTGAGAAAGTGAATATGCGAAACGATCAGTATGATGAAGAAACTTACTCCAA 2151
2161 GAAATTTTGAAGAAAGTGAATATGCGAAGCGACTCAGTATGATGAAGAAACTTACTCCAA 2220
2152 GATCCAAACTTCAATTCATCAATGAAGCAACAGACTTTCATATCTACTTAATGAGCAATCG 2211
2221 GATCCAAACTTCAATTCATCAGTGGGCAATTAAGTTTCGATCCATCGATGGCAATCA 2280
2212 AATTTCAATCTATCCATGAACAAATCTGAACATGGATGGTGGGGAAGTGAGAACATTTACA 2271

2281 AACTTCCCTCTATTAATGAGCTATCTGAACATGATGGTGGGAAGTGCGAATGTTACC 2340
2272 ATCCAGGAGGAATGAGTATTTAAAGAGAAATAGCTCACACTACCGGGGACTTTTAAT 2331
2341 ATTCAAGGAGGAATGAGTATTTAAAGAGAAATTAACGTCACTACCGGGTACTTTTAAT 2400
2332 GAGTGTATCCGAGCTATTTATATCAAAAAATAGGAGAGTCGGAATTAAGAGCTTATACT 2391
2401 GAGTGTATCCAAATTTATATCAAAAAATAGGAGAGTCAGAAATTAAGAGCTTATAGC 2460
2392 CGCTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGATTCGT 2451
2461 CGCTATCAATTAAGAGGGTATATTGAAGATAGTCAAGATCTAGAGATTTATTAATTCGT 2520
2452 TATATCGGAACATGAAACATTCGATGTTCCAGGTACCGAGTCCGTATGCGCGCTTTCA 2511
2521 TACATGCAAAAGCATGAAACATTTGGATGTTCCAGGTACCGATTCCTATGCGCGCTTTCA 2580
2512 GTTGAAGCCCAATCGGAAGGTGCGGAACCGGAATCGATCGCACCACTTTTGAATGG 2571
2581 GTTGAAGCCCAATCGGAAGGTGCGGAACCGGAATCGATCGCACCACTTTTGAATGG 2640
2572 AATCTGATCTAGATTTGTTCTCTGAGAGATGGAGAAATGTGGGCATCATTTCCCATCAT 2631
2641 AATCTGATCTAGATTTGTTCTCTGAGAGATGGAGAGATGTGGGCATCATTTCCCATCAT 2700
2632 TTCTCTTGGATATTTGATTTGGAATGACACACTTGCATGAGATCTTAGGCGTGGGTG 2691
2701 TTCACTTTGGATTTGATTTGTTGGGTGCAACACTTGCATGAGAACCTTAGGCGTGGGTG 2760
2692 GTATTTCAAGATTAAGACGCGAGAAAGTTCATCAAGACTTAGGGAATCTCGAAATTTATGAA 2751
2761 GTATTTCAAGATTAAGACGCGAGAAAGTTCATCAAGATTTAGGAATTTAGGAATTTATCGAA 2820
2752 GAGAAACCAATTTATAGGAGAAAGCACTGCTCTGTTGAGAGAGAGAGAGAGAGAGAGAGAG 2811
2821 GAGAAACCAATTTATTTGGAGAGCACTGCTCTGTTGAGAGAGAGAGAGAGAGAGAGAGAG 2880
2812 GACAAACGTTGAAACCTACAAATTCGNAACAAACGAGTATATACAGAGGCAAGAGAGCT 2871
2881 GACAAACGTTGAAACCTACAAATTCGNAACAAACGAGTATATACAGAGGCAAGAGAGCT 2940
2872 GTGATGCTTTATTTGTAGATTTCTCAATATATAGATTTCAAGGAGATACAAACATTTGCG 2931
2941 GTGATGCTTTATTTGTAGATTTCTCAATATGATCAATTTCAAGGCGGATACAAACATTTGCG 3000
2932 ATGATTCATGCGGAGATPAAACTTTGTTTCATCGAAATTCGAGAGGCTTATCTGTGAGAAATTA 2991
3001 ATGATTCATGCGGAGATPAAACTTTGTTTCATCGAAATTCGAGAGGCTTATCTTTTCAGAAATTA 3060
2992 TCTGTTATCCCGGTGTAAATGCGGAATTTTTCGAAAGATTTAGAGGTCGATTTATCACT 3051
3061 CTTGTTATCCCGGTGTAAATGCGGAATTTTTCGAAAGATTTAGAGGTCGATTTATCACT 3120
3052 GCAATCTCCCTATACGATGCGAGAAATGCTGTTTAAATTCGATTTTAAATTCGATTA 3111
3121 GCAATGCTCTTATACGATGCGAGAAATGCTGTTTAAATTCGATTTTAAATTCGATTA 3180
3112 GCATGCTGGAATGTAAAGGCGATGTAGATGTAACAAGAGCCATTCACCGTTCGTCTCT 3171
3181 ACATGTTGGAATGTAAAGGCGATGTAGATGTAACAAGAGCCATTCATCGTTCGACCTT 3240
3172 GTTATCCAGAGATGGAGAGCAAGATGTCAACAGAGTTCGCGTCTGTCGCGGGCGTGGC 3231
3241 GTTATCCAGAGATGGAGAGCAAGATGTCAACAGAGTTCGCGTCTGTCGCGGGCGTGGC 3300
3232 TATATCTCTCGTGTCAACAGCTTACAAAGAGGATATGAGAGGGTGTGTGAACGATTCAT 3291
3301 TATATCTCTCGTGTCAACAGCTTACAAAGAGGATATGAGAGGGTGTGTGAACGATTCAT 3360
3292 GAAATCGAGAACAAATACAGAGCAACTAAAAATTTAAAAATCTGTGAAGAGAGAGAGTGTAT 3351

Db 3361 GAATCGAGACATACACAGCACTAAATTTAAACCTGTGAAGAGAGAGTGTAT 3420
QY 3352 CCAACGGATACAGGAACGTGTAATGATATATCTGCACACCAAGGTACAGCATGTGTAAT 3411
Db 3421 CCAACGGATACAGGAACGTGTAATGATATATCTGCACACCAAGGTACAGCATGTGTAAT 3480
QY 3412 TCCGTAATGCTGGATATGAGGATGATATGAGTTGATCTACAGCATCTGTTAATTAC 3471
Db 3481 TCCGTAATGCTGGATATGAGGATGATATGAGTTGATCTACAGCATCTGTTAATTAC 3540
QY 3472 AAACCCACTTATGAGAGAGAAAGCTATACAGATGTACGAAGAGATAATCATTTGTGAATAT 3531
Db 3541 AAACCCACTTATGAGAGAGAAAGCTATACAGATGTACGAAGAGATAATCATTTGTGAATAT 3600
QY 3532 GACAGAGGGTATGTGAATATCCACCACTACCGAGTGGTTATATGACAAAAAGAAATTAGAA 3591
Db 3601 GACAGAGGGTATGTGAATATCCACCACTACCGAGTGGTTATATGACAAAAAGAAATTAGAA 3660
QY 3592 TACTTCCAGAAACCGAATAGGTATGGATTGAGATTGGAGAAACCGAAGGAAGTTTATT 3651
Db 3661 TACTTCCAGAAACCGAATAGGTATGGATTGAGATTGGAGAAACCGAAGGAAGTTTATT 3720
QY 3652 GTAGACAGCTGGAATTTACTCTTATGGAGGAATAG 3687
Db 3721 GTAGATAGCTGGATCTACTCTCATGGAGAAATAG 3756

RESULT 10
US-08-881-340-3
; Sequence 3, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cvET4 AND cvET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; STREET: 1601 Market Street, 36th Floor
; City: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881.340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3934 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 67...3756
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2253...2272
US-08-881-340-3

Query Match 72.9%; Score 2687.2; DB 2; Length 3934;
Besc Local Similarity 83.5%; Pred. No. 0;
Matches 3088; Conservative 0; Mismatches 593; Indels 15; Gaps 3;

QY 1 TTGACTTCAAATAGAGAAAAATGAGAATGAAATATAAATGCTTTATCGAATTCGAGCTGTA 60
Db 67 TTGACTTCAAATAGAGAAAAATGAGAATGAAATATAAATGCTTTATCGAATTCGAGCTGTA 126
QY 61 TCGAATCAATCCACACAATGGATCTATCACCAGATCGCTGATTTAGAGATTTCTTTGTGT 120
Db 127 TCGAATCCCTCCACGCAAAATGAATCTATCACAAGATGCTGCTATTTGAAGATAGCTTGT 186
QY 121 ATAGCCGAGGGGAATAATATCAATCCACTTGTAGCGCATCAACAGTCCAAACGGGTATT 180
Db 187 GTAGCCGAGGTGAACAAATATTGATCCATTGTTAGCGCATCAACAGTCCAAACGGGTATA 246
QY 181 AACATAGCTGTAGAAATACTAGGTGTATTAGCGGTACCGTTTGTGTCGACAAATAGCTAGT 240
Db 247 AACATAGCTGTAGAAATACTAGGTGTATTAGCGGTATTTAGCTGTCGACAACTAGCTAGT 306
QY 241 TTTTATAGTTTTCTTTGTTGGTGAATATATGCGCCGCGCAGAGATCAGTGGGAAATTTTC 300
Db 307 TTTTATAGTTTTCTTTGTTGGGGAATTTAGGCTTAGTGGCAGAGATCCATGGGAAATTTTC 366
QY 301 CTAGAACATGTGCAACAACTTTATAAATCAACAAATAACAGAAAAATGCTAGGAATACGGCA 360
Db 367 CTGGAACATGTAGAACAACTTTATAAGACAAACAGTAACAGAAAAATAGTGGAAATACGGCT 426
QY 361 CTTGCTCGAATTACAAGTTTAGGAGATTCTTTTAGAGCTTATCAACAGTCACTTGAAGT 420
Db 427 ATTGCTCGAATTAGAAGGTCTAGGAAAGAGCTATAGATCTTACCAGCAGGCTCTTGAACCT 486
QY 421 TCGCTAGAAAAACCGTGATGATGCAAGAGAGAGTGTCTTTTATACCAATATATAGCC 480
Db 487 TGGTTAGATAACCGAAATGATCAAGATCAAGAGCATATTCTTGGAGGCTATGTTGCT 546
QY 481 TTAGAACTTTGATTTCTTTAATCGATGCGCTTTTTCGCAATTTAGAAACCAAGAGTTCCA 540
Db 547 TTAGAACTTTGATTTCTTTAATCGATGCGCTTTTTCGCAATTTAGAAACCAAGAGTTCCA 606
QY 541 TTATTAATGCTATATGCTCAAGCTGCAATTTTACACCTATTATTATTGAGAGATGCTCT 600
Db 607 TTATTAATGCTATATGCTCAAGCTGCAATTTTACACCTATTATTATTGAGAGATGCTCT 666
QY 601 CTTTGTGTAGTGAATTTTGGGCTTTACATCGCAGGAAATTTCAACGTTATTATTGAGCGCCAA 660
Db 667 CTTTGTGTAGTGAATTTTGGGGAATGGGGAATGGCAUCTTCGATGTTAA CCAATATTACCAAGAACAA 726
QY 661 GTGGAACAAACGAGAGATTATTCCGACTATTGCTAGAGATGTTATTAATACAGTCTAAAT 720
Db 727 ATCAGATATACAGAGGAATAATTCTAACCAATTGCGTACAAATGGTATTAATACAGGGCTAAAT 786
QY 721 AGCTTGAGAGGACAAATCCGCAAGTTTGGGTCGTTTATAATCAATCCGTAGAGATCTA 780
Db 787 AACTTAAGAGGGGCAAAATGCTGAAAGTTGTTGCGGTATAAATCAATTCGTAGAGACCTA 846
QY 781 ACCTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACACTCGCACTTATCCA 840
Db 847 ACCTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAGCTATGACTACTCGCACTTATCCA 906
QY 841 ATAAATACGAGTGTCTCAGTTTAAACAGGGGAAGTTTATACAGCCAAATTTGAGAACACAGG 900
Db 907 ATCAATACGAGTGTCTCAGTTTAAACAGAGAAATTTTATACAGATCCAAATTTGGGAGAACAAAT 966
QY 901 GTAAAT-----ATGCCAGTATGAATTTGTTATAAATAATGCACCTTCGTTTTCGGCT 954

Db 967 GCACCTTCAGGATTTGCAAGTACGAATTGGTTTAATAATAATGACCACTGGTTTTCTGCC 1026
Qy 955 ATAGAGACTCGCGTTATCCGAAGCCCGCATCTACTTGTGATTTTCTAGAAACAACCTCAAAAT 1014
Db 1027 ATAGAGGCTGCCATTTTCAGGCTTCGGCATCTACTTGTGATTTTCCAGAACAACTTACAAAT 1086
Qy 1015 TTATGACCTTCATCAGATGGAAGTGTACTAGGCATATGACTTACTGGGGGGGACACA 1074
Db 1087 TACAGTGCAATCAAGCGTGTGGAGTAGCACTCAACATATGAATTAATGGGTGGGACATAGG 1146
Qy 1075 ATTCAATCTCGGCCAATAGGAGCGGATTAATACTCAACGCAATGGGTCTACCA--AT 1131
Db 1147 CTTAATCTCGGCCAATAGGAGGACATTAATACTCAACAAGGACTTACTTAATAAT 1206
Qy 1132 ACTTCTATTAATCTGTGAAGATTAATCTTCTCTCGAGAGGTATATGGACTGAATCA 1191
Db 1207 ACTTCAATTAATCTGTGAACATTAAGTTTACGTTTACGTTCTCGAGAGGTTTATAGAACAGATCA 1266
Qy 1192 TATGAGAGTGCTCTATAGGGAATTTTACCTTTGAACCTATTTCAATGGTGTCTTACTGTT 1251
Db 1267 AATGACAGGACAAATAT-----ACTATTTTACTCTCTGTGAAATGGAGTAGCTTGGGCT 1320
Qy 1252 AGATTTAATTTTATAGAACCTCAGAAATCTTTTGAAGAGGTACTGCTAACTATAGTCAA 1311
Db 1321 AGATTTAATTTTATAAACCTCAGAAATATTTATGAAGAGGGCCCACTACCTACAGTCAA 1380
Qy 1312 CCTATAGTACACTGGGCTTCAATTAAGAAGATTCAGAAATCAGAAATACCAACAGAAACA 1371
Db 1381 CGGTATCAGGAGTTGGGATTCAAATTTTGAATTCAGAAATCTGAATTAACCAAGAAACA 1440
Qy 1372 ACAGAACGACCAATATGAATCATATAGTCTATAGGTTATCTCAATAGGGCTCAATTTCA 1431
Db 1441 ACAGAACGACCAATATGAATCATATAGTCTATAGTATATCTCATATAGGACTAATCATAT 1500
Qy 1432 CAATCTAGGCTGATGACAGTACCAATATCTTTGGAGCGACCGTAGTGCAGATCGTACAAAT 1491
Db 1501 GGAACACCTTGAGAGCACCTGATTTCTTTGGAGCGATCGTAGTGCAGATCGTACGAAT 1560
Qy 1492 ACCATTAGTTCAGATAGCATAAACAATAACATTTGGTAAATCAATCAACCTTAATTTCA 1551
Db 1561 ACGATTGGACCAATATAGAAATTAACAATAACATTTGGTAAAGCACTGAATCTTCAATTTCA 1620
Qy 1552 GGTACTCTGTAGTCAAGTGGCCAGATTTTACAGAGGGGATATTAATCCGAACCTAAACGTT 1611
Db 1621 GGTGTACTGTGTGGAGGGCCAGATTTTACAGGTGGGGATATCTCTCGTAGAACAAAT 1680
Qy 1612 AATGCTAGTGTACTAAGTATGGTCTTAATTTTAATAATACATCAATTAACAGGGTATCGC 1671
Db 1681 ACGGTACATTTGGAGATATACGATTAATAATATTAATGTGCCATTAATCCCAAGATATCGC 1740
Qy 1672 GTGAGAGTTCTGTATGCTGCTTCTCAACAATGGTCTCGAGGGTAACTGTCCGAGGGAGT 1731
Db 1741 GTAAGATTTGGTTATGCTTCTACTACAGATTTACAAATTTTTCACGAGAAATTAATGGAACC 1800
Qy 1732 ACTACTTTTGATCAAGAGATTCCTTAGTACTATAGTGCAAATAGTCTTTGACATCTCAA 1791
Db 1801 ACTGTTAATATTTGGTAAATTTCTCAAGAATAATGAATAGGGGGAATAATTAAGATATAGA 1860
Qy 1792 TCAATTAAGTTGCAAGATTTCTGTAGGTATAGTGCATCTGGGAGTCAAACTGCTGGA 1851
Db 1861 AGTTTTGAACCTGCAAGATTTAGTACTCTCTTTTAATTTTTTAAATGGCCCAAGCAATTC 1920
Qy 1852 ATAAGTATAAGTAAATAGCAGGTAGACAAAGCTTTTCACTTTGATAAAATTTGAATTCATTT 1911
Db 1921 ACATTTGGGTCTCAGAGTTTTTCAATCAGGAGTTTTATATAGATAGAGTGCATTTGTT 1980
Qy 1912 CCAATTAATGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGGCCGAAGCGCGTGAAT 1971
Db 1981 CCAGCAGAGGTAAACATTTTGGAGCAGATATGATTTAGAAAGAGCACAAGAGCGCGTGAAT 2040
Qy 1972 GCTCTGTTTACTAATACGAATCCAGAGATTTGAACAGATGTCAGAGATTAATCATATT 2031
Db 2041 GCTCTGTTTACTTCTACAAATCCAAAGAGATTTGAAGAGTGTGACAGATTAATCATATT 2100

Qy 2032 GATCAAAGTATCCAATTTAGTGGCGTGTATTCGGATGAATTTCTGCTTAGATGAAAGAGA 2091
Db 2101 GACCAAGTGTCCAATATGCTGGCATGTTTATCAGATGAATTTTCTGCTGATGAGAAGCGA 2160
Qy 2092 GAAATTAATTTGAGAAAGTGAATATGCGAAACGACTCAGTGATGAAGAAACTTACTCCAA 2151
Db 2161 GAAATTAATTTGAGAAAGTGAATATGCGAAAGCGACTCAGTGATGAAGAAACTTACTCCAA 2220
Qy 2152 GATCAAACTTTCACATCCATCAATAAGCAACGAGACTTTCATATCTACTAATGAGCAATCG 2211
Db 2221 GATCAAACTTTCACATTCATCAGTGGGCATTAAGTTTCGCATCCATCGATGGAACATCA 2280
Qy 2212 AATTTTCACATCTATCCATGAACAATCTGAACAATGAGTGGTGGGAAAGTGAGAACTTACA 2271
Db 2281 AACTTCCCTCTATTAATAGACTATCTGAACAATGAGTGGTGGGAAAGTGCGAATGTTACC 2340
Qy 2272 ATCAGGAGAGAAATGAGCTATTTTAAAGAGAAATTTACGTCAACTACCCGGGACTTTTAAT 2331
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Qy 2332 GAGTGTATCCGAGCTATTTATATCAAAAATAGAGAGTCCGAAATTTAAAGCTTATACT 2391
Db 2401 GAGTGTATCCAAATTTATATCAAAAATAGAGAGTCCGAAATTTAAAGCTTATAGC 2460
Qy 2392 CGCTACCAATTAAGAGGGTATATTAAGAGATAGTCAAGATTTTAGAGATATATTTGATTCGT 2451
Db 2461 CGCTATCAATTAAGAGGGTATATTAAGAGATAGTCAAGATTTTAGAGATATATTTAATTCGT 2520
Qy 2452 TATTAATGGGAAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGATAGCGCGCTTTCA 2511
Db 2521 TACAATGCAAGCATGAAACATTTGGATGTTCCAGGTACCGATTTCCCTATGCGCGCTTTCA 2580
Qy 2512 GTTCAAAAGCCCAATCGGAGGTGCGGAAACCGAATCGATCGGACCACTTTTGAATGG 2571
Db 2581 GTTGAAGCCCAATCGGAGGTGCGGAAACCAATCGATCGGACCACTTTTGAATGG 2640
Qy 2572 AATCCTGATCTAGATTTGTTCTCGAGAGATGGAGAAATTTGCGCATCATTTCCCATCAT 2631
Db 2641 AATCCTGATCTAGATTTGTTCTCGAGAGATGGAGAAAGATGTCGCGCATCATTTCCCATCAT 2700
Qy 2632 TTCTCTTTGGATATGATATTTGGATGCAAGACTTTGATGAGAAATCTTAGGCGTGTGGTG 2691
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Qy 2692 GTATTTCAAGATTAAGACGCGAGAGGTCTCCAGACTTAGGGAATCTCGGAATTTATTTCGA 2751
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Qy 2812 GACAAACGTGAAACATCAAAATGCGAAACAAAACGAGTATATACAGAGCGCAAGAGAGCT 2871
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Db 2941 GTGAGCTGTTTATTTGTAGATTTCTCAATATATGATCAATTTACAAGCGGATACAAACATTCGC 3000
Qy 2932 ATGATTCATCGCGCAGATTAATCTGTTTCATCGAATTCGAGAGGCTTATCTCTCGAGAAATTA 2991
Db 3001 ATGATTCATCGCGCAGATTAATCTGTTTCATCGAATTCGAGAGGCTTATCTTTTCAGAAATTA 3060
Qy 2992 TCTGTTATCCCGGTGTAATGCGGAAATTTTGAAGATTTAGAGGTTCGCAATTTACT 3051
Db 3061 CCTGTTATCCCGGTGTAATGCGGAAATTTTGAAGATTTAGAGGTTCGCAATTTACT 3120
Qy 3052 GCAATCTCCCTATACGATGCGAGAAATGTCGTTTAAATGCTGATTTTAAATGAGATTA 3111
Db 3121 GCAATGCTCTTATACGATGCGAGAAATGTCGTTTAAATGCTGATTTTAAATGAGATTA 3180

3112 GCATGCTGGAAATGAAAGGGCATGTAGATGTACAAACAGAGCCATCACCGTTCTGTCTCTT 3171
3181 ACATGTTGGAATGAAAGGGCATGTAGATGTACAAACAGAGCCATCATCGTTCTGACCTT 3240
3172 GTTATCCAGAAATGGGAAGCAAGTGTACAAAGCAAGTTCGGCTGTCTCGGGGGGTGGC 3231
3241 GTTATCCAGAAATGGGAAGCAAGTGTACAAAGCAAGTTCGGCTGTCTCGGGGGGTGGC 3300
3232 TATATCTCTCGTGTACAGAGGTACAAAGAGGGGATATGGAGAGGGTGTGTACGATCCAT 3291
3301 TATATCTCTCGTGTACAGAGGTACAAAGAGGGGATATGGAGAGGGTGTGTACGATCCAT 3360
3292 GAAATCGAGAACATACAGACGAACCTAAATTTAAAACTGTGGAAGAGAGAGTGTAT 3351
3361 GAAATCGAGAACATACAGACGAACCTAAATTTAAAACTGTGGAAGAGAGAGTGTAT 3420
3352 CCAACGATACAGAGCAAGTGTATGATTTATCTACACCAAGTGTACAGAGTGTATGAT 3411
3421 CCAACGATACAGAGCAAGTGTATGATTTATCTGCAACCAAGTGTACAGAGTGTAT 3480
3412 TCCGTAATGCTGGATATGAGGATGCAATATGAAGTTGATATCACTACAGATCTGTAAATAC 3471
3481 TCCGTAATGCTGGATATGAGGATGCAATATGAAGTTGATATCACTACAGATCTGTAAATAC 3540
3472 AAACCGATATGAAGAGAAAGTGTATACAGATGTACAGAGATTAATCAATCTGTGAATAT 3531
3541 AAACCGATATGAAGAGAAAGTGTATACAGATGTACAGAGATTAATCAATCTGTGAATAT 3600
3532 GACAGAGGATGTGAATTTATCCACCACTACAGCTGTGTATATGACAAAAGAAATAGAA 3591
3601 GACAGAGGATGTGAATTTATCCACCACTACAGCTGTGTATATGACAAAAGAAATAGAA 3660
3592 TACTTCCAGAAACCGATATGAAGTATGATGATGAGATTCGAGAAACGGAAGGAAATTTAT 3651
3661 TACTTCCAGAAACCGATATGATGATGATGAGATTCGAGAAACGGAAGGAAATTTAT 3720
3652 GTAGACGCGTGAATTTACTCTTATCGAGGAATAG 3687
3721 GTAGATACGCTGGAATCTCTCTCATGGAAGAAATAG 3756

RESULT 11
US-08-040-751-4
; Sequence 4, Application US/08040751
; Patent No. 5407825
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M
; APPLICANT: Sick, August J
; TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
; TITLE OF INVENTION: active against Lepidopteran Pests and Genes Encoding No. 54078
; TITLE OF INVENTION: Lepidopteran-active toxins
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,751
; FILING DATE: 19930329
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIWANCHIK, DAVID R.
; REFERENCE/DOCKET NUMBER: MA39.C1.D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800
TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: aizawai
; INDIVIDUAL ISOLATE: PS81A2
; IMMEDIATE SOURCE:
; LIBRARY: Lambdagem - 11 (tm) Library of August Sick
; CLONE: 81A2
; US-08-040-751-4

Query Match 48.6%; Score 1793.4; DB 1; Length 3522;
Best Local Similarity 71.9%; Pred.No. 0;
Matches 2497; Conservative 0; Mismatches 861; Indels 117; Gaps 7;

QY 228 ACAATAGCTAGTCTTTTATAGTCTTTTCTGTTGGTGAATTTATGGCCCGCGGAGAGATCA 287
DB 147 ACTAGGGGATTTTACTTGGCTTGTGATGTAATATGGGGGCTATAGGTCCTTCACA 206
QY 288 GTGGGAAATTTCTTAGAACATGTGCAACAACTTATTAATCAACAATAACAGAAATATGC 347
DB 207 ATGGGATATTTTATAGAGCAAAATGAGCTATGATCGGCCCAAGAGATAGAGGAATTCG 266
QY 348 TAGGAATACGGCACTTGTCTGATTAACAGGTTTACGAGATTCCTTTAGAGCCTATCAACA 407
DB 267 TAGGAATACGGCACTTGTCTGATTAACAGGTTTACGAGATTCCTTTAGAGCCTATCAACA 326
QY 408 GTCACTTGAAGATTTGGCTAGAAAACCGTGATGATGATGATGATGATGATGATGATGATG 467
DB 327 TCGTTTAAATAACTGGGAGTAGATCTTACTTAATCCAGCATTAAGAGAAGAGATGCGTAT 386
QY 468 CCAATATATAGCTTTAGAACTTTGATTTCTTAATCGGATCGCGCTTTTCGCAATTAGAAA 527
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QY 528 CCAAGAAATTTCCATTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 587
DB 447 TTATGAATTTCTCTTTTATCAGTATGATGATGATGATGATGATGATGATGATGATGATG 506
QY 588 GAGAGATGCTCTCTTTTGGTGGTGAATTTGGGCTTATCATCGAGGAAATTCACAGTTA 647
DB 507 GAGAGATGTTTCAGTGTGTTGGACACGTTGGGGATTTGATGTAGCAACAATCAATAGTCG 566
QY 648 TTATGAGCCCAAGTGGGAACAAACGAGAGATTTTCCGACTATTCGCTAGAGATGATGATG 707
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QY 3630 AGAAACGGAAGGAAGTTTATTTAGACACCGTGGAAATTAATCTCTTATGGAGGAA 3684
DB 3468 AGAAACGGAAGGAAGTTTATTTAGACAAATGTCGAATTAATCTCTTATGGAGGAA 3522

RESULT 12

US-08-291-368-1
; Sequence 1, Application US/08291368
; Patent No. 5686069
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 5686069el Bacillus thuringiensis Isolates
; TITLE OF INVENTION: Active Against Lepidopteran Pests
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,368
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/597,607
; FILING DATE: 15-OCT-90
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA50.C1
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: aizawai
; INDIVIDUAL ISOLATE: PS81A2
; IMMEDIATE SOURCE:
; LIBRARY: Lambdagem - 11 (tm) Library of August Sick
; CLONE: 81A2
; US-08-291-368-1

Query Match 48.6%; Score 1793.4; DB 1; Length 3522;
Best Local Similarity 71.9%; Pred. No. 0; Mismatches 861; Indels 117; Gaps 7;
Matches 2497; Conservative 0;

QY 228 ACAAAATAGCTAGTCTTTTATAGTTTCTTGTGTGAAATTTATGGCCCGCGGAGATCA 287
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QY 288 GTGGGAATTTCTCTAGAACATGTGCAACAATTTATTAATCAACAATTAACAGAAATGC 347
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QY 348 TAGGATACGGCATTGCTCGATTACAGGTTTATGAGATTCCTTTAGAGCCTTATCAACA 407
DB 267 TAGGATACGGCAATTTCTAGATTACAGGGCTTAGCAATCTTTACCGAATTTACACAA 326
QY 408 GTCACCTGGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTCTTTATAC 467
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Qy 2025 TCATATTGATCAAGTATCCAAATTTTATGTCGGCTGTTTATCGGATGAATTTCTGCTAGATGA 2084

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Db 2088 TATTACCAATCCAGAGAGATGACGTATTTCAAGAGAAATTCAGTCACTACACAGGTAC 2147
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Db 3168 GGAAGTGTATCCACGATACAGGAAGTGTATGATTAATCTGCACACCAAGGTACGC 3227
QY 3402 AG-----TATGTAATCCCGTAATGCTGGATATGAGGATGCATATGAAGTTGA 3449
Db 3228 AGGATCCACAGATCATGTATTTCCCGTAATATCAGATATGAGGATGCATATGAAGTGA 3287
QY 3450 TACTACAGCATCTGTTAAATACAAACCGACTTATGAAGAAGAACGATATACAGATGTACG 3509
Db 3288 TACTACAGCATCTGTTAAATACAAACCGACTTACGAAGAAGAAAGGTATACAGATGTACA 3347
QY 3510 AAGAGATAATCATGTGCAATATGACAGAGGGTATGTGAATATCCACCCTACCAAGTGG 3569
Db 3348 AGGAGATAATCATGTGCAATATGACAGAGGGTATGTGAATATCCACCCTACCAAGTGG 3407
QY 3570 TTATATGACAAAAGAAATAGATACTTCCAGAAACCGATAAGGTATGAGATTCGAGATTGG 3629
Db 3408 TTAATGACAAAAGAAATAGATACTTCCAGAAACCGATAAGGTATGAGATTCGAGATCGG 3467
QY 3630 AGAAACGGAAGGAAGTTTATTTAGACAGCGTGGATTAATCTCTTATGGAGGAA 3684
Db 3468 AGAAACGGAAGGAAGTTTATTTAGACAAATGTCGAATTAATCTCTTATGGAGGAA 3522

RESULT 13

US-08-962-190-1
; Sequence 1, Application US/08962190
; Patent No. 5985267
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 5985267el Bacillus thuringiensis Isolates
; TITLE OF INVENTION: Active Against Lepidopteran Pests
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/962,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,368
; FILING DATE:
; APPLICATION NUMBER: 07/597,607
; FILING DATE: 15-OCT-90
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA50.C1

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: aizawai
; INDIVIDUAL ISOLATE: PS81A2
; IMMEDIATE SOURCE:
; LIBRARY: Lambdagem - 11 (tm) Library of August Sick
; CLONE: 81A2
; US-08-962-190-1

Query Match 48.6%; Score 1793.4; DB 2; Length 3522;
Best Local Similarity 71.9%; Pred. No. 0;
Matches 2497; Conservative 0; Mismatches 861; Indels 117; Gaps 7;
QY 228 ACNAATAGCTAGTCTTTTATAGTCTTTCTGTTGGTGAATTTATGCCCCCGCGGAGATCA 287
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QY 288 GTGGGAAATTTTCCTAGAACATGTCGAACAACTTATAAAATCAACAAATACAGAAAATGC 347
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QY 348 TAGGAATACGGCACTTGTCTCGATTACAAGTTTTAGGAGATTCCTTTAGAGCCTTATCAACA 407
Db 267 TAGGAATACGGCAATTTCTTAGATTACAAGGCTTAAGCAATCTTTACCGAATTTTACACAA 326
QY 408 GTCACTTGAAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAAGTGTCTTTTATAC 467
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QY 468 CCAATATATAGCCTTAGAACTTGATTTCTTAATGGATGCCGCTTTTCGCAATTAGAAA 527
Db 387 TCATTTAATGACATGAACAGTGCCTTACACACAGCTATTTCTCTTTTTCAGTTCAGG 446
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1068 TAATCTATTTTATAGAACACTATCAGACCCCTTCTTCCGAAGATCCGATAATATTATGCC 1127
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1242 TGAGAAATTCATTTAGTTGGATATAGTCATAGATTAAGTCACTGTTAAATTAACCAAGTCT 1301
1425 CATTTTCACAATCTAGGGTCATGTACCAGTATATTCTGGACGCCAGGTAGTGCAGATCG 1484
1302 ATATTAATACTAATAATATAGCTTGGCAACATTTGTTGGACACATCACAGTGTACTGA 1361
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1482 TAACTGTAATGTAGTGTACTAAGTATGAGTCTTAATTTTAAATAATCATCATTAACAGCG 1541
1665 GTATCCGCTGAGAGTTCGTTATGTCTCTCAAAATGGTCTCTGAGGGTAACTGTGCG 1724
1542 GTATCCGCTGAGAGTTCGTTATGTCTCTCAAAATGGTCTCATGAGAGTAAATGTTGG 1601
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1602 AGGGAGTACTACTTTTGTATCAAGGATTCCTAGTACTATGAGTCAAAATGAGTCTTTGAC 1661
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1662 ATCTCAATCATTTAGATTTGAGAAATTTCTCTAGGCAATTTAGTATCTGGCAGTCAAC 1721
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1722 TGCTGGAATAAGTATAAGTAAATAGCAGGTAGACAAACGTTTCACTTTAGATGAAATTTGA 1781
1905 ATTCAATTCGAATTTACTGCAACCTTCGAGAGCAATACGATTTAGAAAGGGCGCAAGGCG 1964
1782 ATTTATCCAGTGTGATGCAACATTTTGAAGCAGAAATAGATTTAGAAAGAGCACAAAGGC 1841
1965 GGTGAATGCTCTGTTTACTTAATACGAATTCAGAGATTTGAAACAGAGATGTGACAGATTA 2024
1842 GGTGAATTCGCTGTTTACTTCTTCGAATTCAGATTTGAAACAGAGATGTGACAGATTA 1901
2025 TCATATTGATCAAGTATCCAATTTTAGTGGCGTGTATTATCGGATGAATTTCTGCTTAGATGA 2084

1902 TCATATTGATCAAGTATCCAATTTTAGTAGATTGTTATCCGATGAATTTGTCTGATGA 1961
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1962 AAAGCAGAAATTTGTCCGAGAAAGTCAAAACATGCGAAGCGACTCAGTGTATGAGCGGAA 2021
2145 ACTTCAAGATCCAAATTTTCACTCATCAATAAGCAACAGACTTTTCAATCTCTACTAATGA 2204
2022 ACTTCAAGATCCAAATTTTCAAGGGATCAATAGGCAACAGAC----- 2064
2205 GCAATCGAATTTTCACTCATCTATCCATGAACAATTCGAACATGATGGTGGGGAAGTGAGAA 2264
2065 -----CGTGGCTGGAGAGGAAGTACGGA 2087
2265 CATTACATCCAGGAGGAAATGAGTATTTTAAAGAGAAATTTACGTCACTACCCGGGAC 2324
2088 TATTACCATCCAGAGGAGGATGACGTATTCAGAGAGAAATTTACGTCACTACCAAGGTAC 2147
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2148 CTTTGTAGTGTCTATCCAGCTATTTGTATCAAAAAATAGATGAGTCCGAAATTTAAAGC 2207
2385 TTATATCTCGTACCAATTTAAGAGGCTATTTTGAAGATAGTCAAGATTTTAGAGATATATTT 2444
2208 CTATAACCGTTTACCAATTTAAGAGGCTATTCGAAGATAGTCAAGACTTTAGAAATCTATTT 2267
2445 GATTGCTTATTAATGGGAAACATGAACATTTGGATGTTTCCAGGTACCGAGTCCGTATGGCC 2504
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2328 GCTTTCAGTTCGAAAGTCCAAATTTGGAAGTGGGAGAACCGAATCGGTGTGCGCACACT 2387
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2388 TGAATGGAATCCTGATTTAGATTGTTCTCGCAGAGACGGGGAATAATGTCACATCATTC 2447
2625 CCATCATTTCTTTGGATTTGATTTGGATGACAGACTTTGCATGAGAAATCTAGGGCT 2684
2448 CCATCATTTCTTTGGACATTTGATTTGGATGACAGACTTTGCAAGAGGATCTAGGGCT 2507
2685 GTGGGTGTATTTCAAGATTAAAGACGAGGAGGTCTGCAAGACTTAGGGAATCTGGAAT 2744
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2805 ATGAGAGACAAACGTTGAAAACTCAATTTGGAAAAACAAACAGATATATACAGAGGCAAA 2864
2628 ATGAGAGACAAACGTTGAAAACTCAATTTGGAAAAACAAACAGATATATACAGAGGCAAA 2687
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2888 AGAAGCTGTGATGCTTTTATTTGTAGATTTCTCAATATAATAGATTACAAAGCGATACAAA 2747
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2808 AGAATACCTTTTCAATTCAGGAATAAATTTGTTGTTGTTTGAAGAAATTTAGAAAAACCGTAT 2867
3045 TATCACTGCATCTCCCTTATACGATGCGAGAAATGTCGTTTAAATGTCGTTAAATGTCGTTTAA 3104
2868 TTCTACTGCATTTATCCCTTATATGATGCGAGAAATGTCATTTAAATGTCGTTTAAATGTCGTTTAA 2927
3105 TGGATTAGCATGCTGGAATGTAAAGGCGCATGTAGAT---GTACAAACAGAGCCATCACCG 3161

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Db 2928 TGGCTTATCATCTGGAACCGTGAAGGCGCATGTAGTAGTAGTGAACAAAAACCAACCG 2987
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Qy 3222 GGGCGTGGCTATATCTCCGTGTCAAGCGTACAAAGAGGGATATGGAGAGGTTGTGT 3281
Db 3048 GGGCGTGGCTATATCTCCGTGTACAGCGTACAAAGAGGGATATGGAGAGGTTGCGT 3107
Qy 3282 AAGATCCATGAATCGAGAACATACAGACGAACATAAATTTAAACCTGTGAAGAAGA 3341
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Qy 3342 GGAAGTGTATCCACGATACAGGAAGCTGTATGATGATATCTGCAACCAACGATACAGC 3401
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Db 3228 AGATCCACAGATCATGTAAATCCCGTAAATATACAGATGAGGATGCAATGAAAGTTGA 3287
Qy 3450 TACTACAGATCTGTTAAATACAAACCGACTTATGAAGAAGAAACGTTATACAGATGTACG 3509
Db 3288 TACTACAGATCTGTTAAATACAAACCGACTTATGAAGAAGAAAGGTATACAGATGTACA 3347
Qy 3510 AAGGATAAATCTGTGAATATGACAGAGGATATGTAATATCCACCACTACAGCTGG 3569
Db 3348 AGGAGATAATCTGTGAATATGACAGAGGATATGTAATATCCACCACTACAGCTGG 3407
Qy 3570 TTATATGACAAAGAAATAGAAATCTCCAGAAACCGATAAGGTATGAGATTGAGATTGG 3629
Db 3408 TTATGTCAGAAAGAAATAGAGTACTTCCAGAAACCGATAAGGTATGAGATTGAGATTGG 3467
Qy 3630 AGAAACGGAAGGAGTTTATGTAGACAGCGTGAATTAATCTCTTATGGAGAA 3684
Db 3468 AGAAACGGAAGGAGTTTATGTAGACAAATGTCGAATTAATCTCTTATGGAGAA 3522
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RESULT 14

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PCT-US95-10310-1
; Sequence 1, Application PC/TUS9510310
; GENERAL INFORMATION:
; APPLICANT: MYCOGEN CORPORATION 5501 Oberlin Drive
; APPLICANT: STREET ADDRESS:
; APPLICANT: CITY: San Diego
; APPLICANT: STATE/PROVINCE: California
; APPLICANT: COUNTRY: US
; APPLICANT: POSTAL CODE/ZIP: 92121
; APPLICANT: PHONE NUMBER: (619) 453-8030
; APPLICANT: FAX NUMBER: (619) 453-6991
; TITLE OF INVENTION: Protein Toxins Active Against Lepidopteran Pests
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10310
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/597,607
; FILING DATE: 15-OCT-90
; CLASSIFICATION:
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; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MAS0.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORGANISM: Bacillus thuringiensis
; STRAIN: aizawai
; INDIVIDUAL ISOLATE: PS81A2
; IMMEDIATE SOURCE:
; LIBRARY: Lambdaem - 11 (tm) Library of August Sick
; CLONE: 81A2
; PCT-US95-10310-1
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Query Match 48.6%; Score 1793.4; DB 5; Length 3522;
Best Local Similarity 71.9%; Pred. No. 0;
Matches 2497; Conservative 0; Mismatches 861; Indels 117; Gaps 7;

Qy 228 ACAATAGCTAGCTTTTATAGTTTCTTCTGTTGTAATTTATGGCCCGCGCAGAGATCA 287
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Qy 288 GTGGGAATTTTCCTAGAACATGTGCAACAACCTTATAAATCAACAATTAACAGAAATGC 347
Db 207 ATGGGATATATTTTATAGAGCAAAATTGAGCTATTGATCGCCCAAGAAATAGAGGAATTCGC 266
Qy 348 TAGGAATACGGCACTTGTCTCGATTACAAGTTTATGAGAGATTCCTTTAGAGCCTTATCAACA 407
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Qy 408 GTCATTTGAAGATTTGGCTAGAAACCGTGATGATGCAAGAACGAGAAAGTGTCTTTATATAC 467
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Qy 528 CCAAGAAAGTTCCATTTAATTAATGATATGCTCAAGCTGCAAAATTTACACCTATTATTATT 587
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Qy 588 GAGAGATGCTCTCTTTTGGTAGTGAATTTGGGCTTACATCCAGGAAATTCACAGTTA 647
Db 507 GAGAGATGTTTCAGTGTTTGGACAACGTTGGGGATTTGATGTAGCAACAATCAATAGTCG 566
Qy 648 TTATGAGCGCAAGTGGAAACAAACGAGAGATTTATCCGACTATTGCGTAGAATGGTATAA 707
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Qy 708 TACAGGTCTAAATAGCTTCGAGAGGGACAATAGCCG--CAAGTTGGTGGTTTATATCA 764
Db 627 TACGGGTTAAATCGTTTACCAGTAAATGAGGGGTACGAGGATGGCAAGATTTAATAG 686
Qy 765 ATTCCGTAGAGATCTAAACGTTAGGGGTATTAGATCTAGTGGCACTATTCACAGCTATGA 824
Db 687 GTTTAGAGAGAGGTAAACAATATCAGTATTAGATAATTTCTTTTTCACAAATTTACGA 746
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QY 885 AATTGGAGCAACAGGGGTAATAATATGGCAAGTATGAAATGGTATATAATAATAATATGCACTTC 944
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QY 945 GTTTTCGGCTATAGAGACTGGGTTATCCGAAGCCGGATCTACTGTTGATTTCTTGAACA 1004
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QY 1005 ACTTACAATTTTAGCACCTTCATCAGATGGAGTCTACTAGGCATATGCACTTACTGGCG 1064
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Db 1542 GTATCGGTGAGAGTTGTTATGCTGCTTCAAAATGTCCTGAGGATTAATGTTGG 1601
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QY 1905 ATTCATTCCTCAATTTACTGCAACCTTCGAAGCAGAAATACGATTTAGAAAGGGCGCAGAGC 1964
Db 1782 ATTTATCCAGTTGATGCAACATTTGAAGCAGATATGATTTAGAAAGACACAAAAGGC 1841
QY 1965 GGTGAATGCTCTGTTTACTAATACGAATCCAGAAGATTGAACACAGATGTGACAGATTA 2024

Db 1842 GGTGAATTCGCTGTTTACTTCTTCAATCAAAATCGAGTTAAAAACAGATGTGACGATTA 1901
QY 2025 TCATATTGATCAAGTATCCAAATTTAGTGGCGCTGTTTATCGGATGAAATTTCTGCTTATAGA 2084
Db 1902 TCATATTGATCAAGTATCCAAATTTAGTATGTTTATCCGATGAAATTTTGTCTGATGA 1961
QY 2085 AAAGAGAGAAATTAATTGAGAAAGTGAATAATGCGAAACGACTCAGTGTATGAAGAAACTT 2144
Db 1962 AAAGGAGAAATTTCCGAGAAAGTCAACATGCGAAGGACTCAGTGTATGAGCGGAAATTT 2021
QY 2145 ACTCAAGATCCAAACTTTCACATCCATCAATTAAGCAACACGACTTTCATATCTACTAATGA 2204
Db 2022 ACTTCAAGATCCAAACTTTCAGAGGATCAATAGGCAACGAC----- 2064
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Db 2065 -----CGTGGCTGGAGAGGAAGTACGGA 2087
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Search completed: November 21, 2004, 16:55:54
Job time : 355 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 08:55:06 ; Search time 1733 Seconds
(without alignments)
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Title: US-10-614-524-1

Perfect score: 3687

Sequence: 1 ttgacttcaaataggaaaaa.....tactcttatggaggaatag 3687

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3666.2	99.4	4173	15	US-10-428-961-37
3	3260.2	88.4	3684	15	US-10-428-961-62
4	3133.6	85.0	3687	17	US-10-809-953-9
5	1581.6	42.9	3558	9	US-09-826-660-22
6	1495.6	40.6	3624	10	US-09-988-462-6
7	1408.4	38.2	3522	9	US-09-826-660-5
8	1408.4	38.2	3522	11	US-09-837-961-7
9	1408.4	38.2	3522	18	US-10-825-751-7
10	1402	38.0	3534	9	US-09-873-873-25
11	1402	38.0	3534	10	US-09-916-956A-25
12	1402	38.0	3534	10	US-09-997-914-25

13	1402	38.0	3534	15	US-10-365-645-25	Sequence 25, Appl
14	1402	38.0	3534	16	US-10-672-163-25	Sequence 25, Appl
15	1402	38.0	3534	17	US-10-739-482-25	Sequence 25, Appl
16	1402	38.0	3534	17	US-10-817-182-25	Sequence 25, Appl
17	1400.6	38.0	3531	9	US-09-873-873-9	Sequence 9, Appl
18	1400.6	38.0	3531	9	US-09-873-873-11	Sequence 11, Appl
19	1400.6	38.0	3531	9	US-09-873-873-13	Sequence 13, Appl
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36	1400.6	38.0	3531	17	US-10-817-182-11	Sequence 11, Appl
37	1400.6	38.0	3531	17	US-10-817-182-13	Sequence 13, Appl
38	1392.4	37.8	3534	9	US-09-873-873-27	Sequence 27, Appl
39	1392.4	37.8	3534	10	US-09-916-956A-27	Sequence 27, Appl
40	1392.4	37.8	3534	10	US-09-997-914-27	Sequence 27, Appl
41	1392.4	37.8	3534	15	US-10-365-645-27	Sequence 27, Appl
42	1392.4	37.8	3534	16	US-10-672-163-27	Sequence 27, Appl
43	1392.4	37.8	3534	17	US-10-739-482-27	Sequence 27, Appl
44	1392.4	37.8	3534	17	US-10-817-182-27	Sequence 27, Appl
45	1390	37.7	3567	10	US-09-972-175-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-614-524-1
; Sequence 1, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Dame, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSU2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3687
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-10-614-524-1

Query Match 100.0%; Score 3687; DB 16; Length 3687;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3687; Conservative 0; Mismatches 0; Gaps 0;
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1441	GTGCATGTACCAAGTATATCTTTCGAG	CGCACCGGTAGTCAGATCGTACAAATAC	CAATTAGT	1500
1501	TCAGATAGCATAAACAAATACCAATGG	TGTAATTCATTCAACCTTAATTCAGGTAC	CTCT	1560
1501	TCAGATAGCATAAACAAATACCAATGG	TGTAATTCATTCAACCTTAATTCAGGTAC	CTCT	1560
1561	GTAGTCAGTGGCCCCAGGATTTACAGG	AGGGATATAATCCGAACTAACTGTTAAT	TGGTAGT	1620
1561	GTAGTCAGTGGCCCCAGGATTTACAGG	AGGGATATAATCCGAACTAACTGTTAAT	TGGTAGT	1620
1621	GTACTAAGTATGGTCTTAATTTTAATA	TATTAATACATCATTAACGGGTATCG	GTGAGATT	1680
1621	GTACTAAGTATGGTCTTAATTTTAATA	TATTAATACATCATTAACGGGTATCG	GTGAGATT	1680
1681	CGTTATGCTGCTTCTCAAAACAATGG	TCTCAGGGTAACTGTCCGAGGGAGTAC	TACTTTTT	1740
1681	CGTTATGCTGCTTCTCAAAACAATGG	TCTCAGGGTAACTGTCCGAGGGAGTAC	TACTTTTT	1740
1741	GATCAAGGATTCCTTAGTACTATGAGT	GCAAAATGAGTCTTTGACATCTCAATCA	ATTTAGA	1800
1741	GATCAAGGATTCCTTAGTACTATGAGT	GCAAAATGAGTCTTTGACATCTCAATCA	ATTTAGA	1800
1801	TTTGCAGAAATTCCTGTAGGTAATTA	TGTGCAATCTGGCAGTCAAACTGCTG	GAATAGTATA	1860
1801	TTTGCAGAAATTCCTGTAGGTAATTA	TGTGCAATCTGGCAGTCAAACTGCTG	GAATAGTATA	1860
1861	AGTAATAATGCAGGTAGACAAAGTTT	CACCTTCATGATAAAATGAAATTCATT	CCCAATTA	1920
1861	AGTAATAATGCAGGTAGACAAAGTTT	CACCTTCATGATAAAATGAAATTCATT	CCCAATTA	1920
1921	GCAACCTTCGAAAGCAGAAATACGAT	TTTAAAGGCGCAAGAGCGGTGAATG	CTCTGTTT	1980
1921	GCAACCTTCGAAAGCAGAAATACGAT	TTTAAAGGCGCGCAAGAGCGGTGAAT	GCTCTGTTT	1980
1981	ACTAATAACGAATCCAAAGAGATTGA	AAAAACAGATGTGACAGATTATCAT	TATTGATCAAGTA	2040
1981	ACTAATAACGAATCCAAAGAGATTGA	AAAAACAGATGTGACAGATTATCAT	TATTGATCAAGTA	2040
2041	TCCAAATTTAGTGGCGTGTATCCGAT	GAATTCCTGCTTAGATGAAAAGAGAA	ATTACTTT	2100
2041	TCCAAATTTAGTGGCGTGTATCCGAT	GAATTCCTGCTTAGATGAAAAGAGAA	ATTACTTT	2100
2101	GAGAAAGTGAAATATGCGAAACGACT	CAGTGATGAAAGAACTTACTCCAAG	ATCCAAC	2160
2101	GAGAAAGTGAAATATGCGAAACGACT	CAGTGATGAAAGAACTTACTCCAAG	ATCCAAC	2160
2161	TTCAATCCATCAATAGCAACGACCTT	CAATCTACTAATAGCAATCGAATTT	CCACA	2220
2161	TTCAATCCATCAATAGCAACGACCTT	CAATCTACTAATAGCAATCGAATTT	CCACA	2220

Qy	2221	TCTATCCATGAA	CAATCTGAAC	ATGGAATCTGGATGGTGGGAAAGTGAGAA	CAATTACAATCCAGGAA	2280		
Db	2221	TCTATCCATGAA	CAATCTGAAC	ATGGAATGGTGGGAAAGTGAGAA	CAATTACAATCCAGGAA	2280		
Qy	2281	GGAATGACG	TATTTAAAGAGAA	TTCGTCACTACCGGGGAC	TTTTAAATGAGTGTTAT	2340		
Db	2281	GGAATGACG	TATTTAAAGAGAA	TTCGTCACTACCGGGGAC	TTTTAAATGAGTGTTAT	2340		
Qy	2341	CCGACG	TATTTATCAAAA	ATAAGGAGGTCCGAA	TTAAAGGTTATACTCGCTACCAA	2400		
Db	2341	CCGACG	TATTTATCAAAA	ATAAGGAGGTCCGAA	TTAAAGGTTATACTCGCTACCAA	2400		
Qy	2401	TTAAGAGGG	TATTTGAAGATAGTCAAGATTTAGAGATATATTTTGATTCGTTATATCGG	2460				
Db	2401	TTAAGAGGG	TATTTGAAGATAGTCAAGATTTAGAGATATATTTTGATTCGTTATATCGG	2460				
Qy	2461	AAACATGAA	ACATTTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTTCAGTTGAAAGC	2520				
Db	2461	AAACATGAA	ACATTTGGATGTTCCAGGTACCGAGTCCGTATGGCCGCTTTTCAGTTGAAAGC	2520				
Qy	2521	CCAA	TCGGAAGGTCGGAGAACCGAA	TCGATGCGCACCA	TATTTGAAATGGAATCCTGAT	2580		
Db	2521	CCAA	TCGGAAGGTCGGAGAACCGAA	TCGATGCGCACCA	TATTTGAAATGGAATCCTGAT	2580		
Qy	2581	CTAGAT	TGTTCC	TCAGAGATGGAGAA	AAATGTCGGCATCATTTCCCATCATTTCTCTTTG	2640		
Db	2581	CTAGAT	TGTTCC	TCAGAGATGGAGAA	AAATGTCGGCATCATTTCCCATCATTTCTCTTTG	2640		
Qy	2641	GATAT	TCGATATGGA	TCGACAGACTTCGATGAGAA	TCTAGCGGTGTCGGTGGTATTCGAAG	2700		
Db	2641	GATAT	TCGATATGGA	TCGACAGACTTCGATGAGAA	TCTAGCGGTGTCGGTGGTATTCGAAG	2700		
Qy	2701	ATTAAG	ACGCGAGGAAGTCTATGCAAGACTAGGGAATCTGAA	TTATTTGAAGAGAA	ACCA	2760		
Db	2701	ATTAAG	ACGCGAGGAAGTCTATGCAAGACTAGGGAATCTGAA	TTATTTGAAGAGAA	ACCA	2760		
Qy	2761	TTAT	TAGGAGAC	CACGTCTCGTGTGAGAGAGCAGAGAA	AAATTCGGAGACAAACGT	2820		
Db	2761	TTAT	TAGGAGAC	CACGTCTCGTGTGAGAGAGCAGAGAA	AAATTCGGAGACAAACGT	2820		
Qy	2821	GAAAA	CTCAATTTG	AAAAACAAACGAGTATATACAGAGGCA	AAAGAGCTGTGGATGCT	2880		
Db	2821	GAAAA	CTCAATTTG	AAAAACAAACGAGTATATACAGAGGCA	AAAGAGCTGTGGATGCT	2880		
Qy	2881	TTAT	TGTTAGATTC	CTCAATATATAGATATACAGCGGATACAA	ACATTTGCGATGATTCAT	2940		
Db	2881	TTAT	TGTTAGATTC	CTCAATATATAGATATACAGCGGATACAA	ACATTTGCGATGATTCAT	2940		
Qy	2941	CGGC	CAGATAAC	CTGTGTTCA	CGAATTCGAGAGCTTATCTGTGAGAA	TTATCTGTTATC	3000	
Db	2941	CGGC	CAGATAAC	CTGTGTTCA	CGAATTCGAGAGCTTATCTGTGAGAA	TTATCTGTTATC	3000	
Qy	3001	CCGG	CTGTAAATG	CGGAAATTTT	TGAAGAA	TTAGAAAGCTCGCA	TTATCACTCTCC	3060
Db	3001	CCGG	CTGTAAATG	CGGAAATTTT	TGAAGAA	TTAGAAAGCTCGCA	TTATCACTCTCC	3060
Qy	3061	CTAT	ACGATGCGAGAA	ATGCTGTTAA	AAATGGTGA	TTTAAATGGA	TTAGCATGCTGG	3120
Db	3061	CTAT	ACGATGCGAGAA	ATGCTGTTAA	AAATGGTGA	TTTAAATGGA	TTAGCATGCTGG	3120
Qy	3121	AATG	TAAAGGG	CATGTAGATGTTACACAGCCATCAC	CGTTCGTGCTGTTGTTATCCCA	3180		
Db	3121	AATG	TAAAGGG	CATGTAGATGTTACACAGCCATCAC	CGTTCGTGCTGTTGTTATCCCA	3180		
Qy	3181	GAAT	TGGGAAG	CAGAA	TGTCAAGCAGTTTCGGGTCTGT	CGGGGGCGTGGCTATATCCTC	3240	
Db	3181	GAAT	TGGGAAG	CAGAA	TGTCAAGCAGTTTCGGGTCTGT	CGGGGGCGTGGCTATATCCTC	3240	
Qy	3241	CGTG	CTCACAG	CGTACAAAGAGGGATATG	GAGAGGGTTGTGTACAGATCCAT	GAAATCGAG	3300	
Db	3241	CGTG	CTCACAG	CGTACAAAGAGGGATATG	GAGAGGGTTGTGTACAGATCCAT	GAAATCGAG	3300	

Qy	3301	AACAAATACAGACGAACTTAAATACTGTGAAGAGAGGAAGTGTATCCAAACGGAT	3360
Db	3301	AACAAATACAGACGAACTTAAATACTGTGAAGAGAGGAAGTGTATCCAAACGGAT	3360
Qy	3361	ACAGGACGCTGTAATGAATTAATCTGCACACCAAGGTACACGACGTATGTAAATTCCTCCGTAAT	3420
Db	3361	ACAGGACGCTGTAATGAATTAATCTGCACACCAAGGTACACGACGTATGTAAATTCCTCCGTAAT	3420
Qy	3421	GCTGGATATGAGGATGCAATGAAGTTTGATATCAACGACATCTCTTAAATTAACAAACCGACT	3480
Db	3421	GCTGGATATGAGGATGCAATGAAGTTTGATATCAACGACATCTCTTAAATTAACAAACCGACT	3480
Qy	3481	TATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTTGTGAATATGACAGAGG	3540
Db	3481	TATGAAGAAGAAACGTATACAGATGTACGAAGAGATAATCATTTGTGAATATGACAGAGG	3540
Qy	3541	TATGTGAATTAATCCACACTACCAGCTGGTTATATGACAAAGAAATAGGAATACTTCCCA	3600
Db	3541	TATGTGAATTAATCCACACTACCAGCTGGTTATATGACAAAGAAATAGGAATACTTCCCA	3600
Qy	3601	GAACCCGATAAGGTATGGAATGGAGATGGAGAAACGGAAGGGAAGTTTATTTGTAGACAGC	3660
Db	3601	GAACCCGATAAGGTATGGAATGGAGATGGAGAAACGGAAGGGAAGTTTATTTGTAGACAGC	3660
Qy	3661	GTGGAATTACTCTCTTATGGAGGAATAG	3687
Db	3661	GTGGAATTACTCTCTTATGGAGGAATAG	3687

RESULT 2

US-10-428-961-37

; Sequence 37, Application US/10428961

; Publication No. US20030237111A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Wei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Rupar, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amend)

; FILE REFERENCES: MESCO201--1

; CURRENT APPLICATION NUMBER: US/10/428,961

; CURRENT FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 09/661,322

; PRIOR FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: 60/153,995

; PRIOR FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 37

; LENGTH: 4173

; TYPE: DNA

; ORGANISM: Bacillus thuringiensis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3687)

US-10-428-961-37

Query Match 99.4%; Score 3665.2; DB 15; Length 4173;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 3674; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy	1	TTGACTTCAAATAGGAAAAATGAGATGAAATATTAATATGCTTTTATCGATTCAGCTGTGA	60
Db	1	TTGACTTCAAATAGGAAAAATGAGATGAAATATTAATATGCTTTTATCGATTCAGCTGTGA	60
Qy	61	TCCGAATCTCCACACAAATGGATCTATCACAGATGCTGTATTCAGGATTCCTTTGTGT	120
Db	61	TCCGAATCTCCACACAAATGGATCTATCACAGATGCTGTATTCAGGATTCCTTTGTGT	120
Qy	121	ATAGCCGAGGGGAATAATATCAATCCACTTTGTAGCGCATCAACAGCTCCAAACGGGTATT	180

Db 121 ATAGCCGAGGGAATAATATCAATCCACTTCTGTAGCGCATCAACAGTCCAAACCGGTATT 180
Qy 181 AACATAGCTGTAGNAATACTAGGTGTATATAGGGGTACCGTTTGTGACAAATAGCTAGT 240
Db 181 AACATAGCTGTAGNAATACTAGGTGTATATAGGGGTACCGTTTGTGACAAATAGCTAGT 240
Qy 241 TTTTATAGTTTCTTGTGGTGAATATATGGCCCGCGCAGAGATCAGTGGGAATTTTC 300
Db 241 TTTTATAGTTTCTTGTGGTGAATATATGGCCCGCGCAGAGATCAGTGGGAATTTTC 300
Qy 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
Db 301 CTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAATGCTAGGAATACGGCA 360
Qy 361 CTTCCTCGATTAACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Db 361 CTTCCTCGATTAACAGGTTTAGGAGATTCCTTTAGAGCCTATCAACAGTCACTTGAAGAT 420
Qy 421 TGGCTAGAAAACCGTGTATGATGCAAGAACGAGAAGTGTCTTTATACCCCAATATATAGCC 480
Db 421 TGGCTAGAAAACCGTGTATGATGCAAGAACGAGAAGTGTCTTTATACCCCAATATATAGCC 480
Qy 481 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAACCAGGAAGTTCCA 540
Db 481 TTAGAACTTGATTTCTTAATGCGATGCGCTTTTCGCAATTAGAACCAGGAAGTTCCA 540
Qy 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATATATTTAGAGAGATGCCCTCT 600
Db 541 TTATTAATGGTATATGCTCAAGCTGCAAAATTTACACCTATATATTTAGAGAGATGCCCTCT 600
Qy 601 CTTTTCCTAGTGAATTTGGCTTACATCGCAGGAATTCAAAGTTTATATAGCCGCA 660
Db 601 CTTTTCCTAGTGAATTTGGCTTACATCGCAGGAATTCAAAGTTTATATAGCCGCA 660
Qy 661 GTGGAAACAAACGAGAGATTTCCGACTATGCGTAGAATGGTATGATGAGATCTA 720
Db 661 GTGGAAACAAACGAGAGATTTCCGACTATGCGTAGAATGGTATGATGAGATCTA 720
Qy 721 AGCTTGAGAGGGAACAAATGCGCAAGTTGGGTGCTTATATCAATTCGCTAGAGATCTA 780
Db 721 AGCTTGAGAGGGAACAAATGCGCAAGTTGGGTGCTTATATCAATTCGCTAGAGATCTA 780
Qy 781 AGCTTGAGGGAATTTAGATCTAGTGGCACTATCCCAAGCTATGACACTCGCACTTATCCA 840
Db 781 AGCTTGAGGGAATTTAGATCTAGTGGCACTATCCCAAGCTATGACACTCGCACTTATCCA 840
Qy 841 ATAAATACGAGTCTCAGTTTAAACAGGGAAGTTTATACAGCCAAATGGAGCAACAGGG 900
Db 841 ATAAATACGAGTCTCAGTTTAAACAGGGAAGTTTATACAGCCAAATGGAGCAACAGGG 900
Qy 901 GTAAATATGCAAGTATGAATTCGTATATAATAATGCACTTCGTTTCCGCTATAGAG 960
Db 901 GTAAATATGCAAGTATGAATTCGTATATAATAATGCACTTCGTTTCCGCTATAGAG 960
Qy 961 ACTGCGGTTATCCGAAGCCGCACTACTGTTGATTTTCTAGAACAACTTACAAATTTTAC 1020
Db 961 ACTGCGGTTATCCGAAGCCGCACTACTGTTGATTTTCTAGAACAACTTACAAATTTTAC 1020
Qy 1021 ACTTCATCAGATGGAGTGTACTAGGCATATGACTTACTGCGGGGGGCAACAATTCAA 1080
Db 1021 ACTTCATCAGATGGAGTGTACTAGGCATATGACTTACTGCGGGGGGCAACAATTCAA 1080
Qy 1081 TCTCGGCCAATAGGAGCGGATTAATACTCAACGATGGGTCTACCAATCTCTATT 1140
Db 1081 TCTCGGCCAATAGGAGCGGATTAATACTCAACGATGGGTCTACCAATCTCTATT 1140
Qy 1141 AATCCTGTAGATTAATCACTTCTCTCGAGAGTATATGAGCTGAATCATATGACGGA 1200
Db 1141 AATCCTGTAGATTAATCACTTCTCTCGAGAGTATATGAGCTGAATCATATGACGGA 1200
Qy 1201 GTGCTTCTATGGGGAATTTACCTTGAACCTTATTCATGGTGTCCCTACTGTTAGATTTAT 1260
Db 1201 GTGCTTCTATGGGGAATTTACCTTGAACCTTATTCATGGTGTCCCTACTGTTAGATTTAT 1260

Qy 1261 TTTTAGAACCCCTCAGAACTACTTTTGAAGAGGTACTGCTAACTATAGTCAACCCCTATGAG 1320
Db 1261 TTTTAGAACCCCTCAGAACTACTTTTGAAGAGGTACTGCTAACTATAGTCAACCCCTATGAG 1320
Qy 1321 TCACCTGGGCTTCAATTAAGAGTTTCAAGAACTGAATTAACCAACGAAACAAACAGAACGA 1380
Db 1321 TCACCTGGGCTTCAATTAAGAGATTCAAGAACTGAATTAACCAACGAAACAAACAGAACGA 1380
Qy 1381 CCAAAATTAAGAACTATATAGTCTATAGTCTACATAGGGCTCATTTTCAACAACTCTAGG 1440
Db 1381 CCAAAATTAAGAACTATATAGTCTATAGTCTACATAGGGCTCATTTTCAACAACTCTAGG 1440
Qy 1441 GTGCATGTACCAAGTATATTTTGGACGACCGTAGTGCAGATCGTACAAATACCAATTAGT 1500
Db 1441 GTGCATGTACCAAGTATATTTTGGACGACCGTAGTGCAGATCGTACAAATACCAATTAGT 1500
Qy 1501 TCAGATAGCATTAACACAAATACCAATTTGGTAAATTCATTCAACCTTTAATTCAGGTACTCT 1560
Db 1501 TCAGATAGCATTAACACAAATACCAATTTGGTAAATTCATTCAACCTTTAATTCAGGTACTCT 1560
Qy 1561 GTAGTCACTGGGCCAGGATTTTACAGGAGGGGATATTAATCCGAACCTAACCTTTAATGCTAGT 1620
Db 1561 GTAGTCACTGGGCCAGGATTTTACAGGAGGGGATATTAATCCGAACCTAACCTTTAATGCTAGT 1620
Qy 1621 GTACTAAGTATGGGCTTAAATTTTAAATATACATCAATTAACAGCGGTATCGCGTAGAGTT 1680
Db 1621 GTACTAAGTATGGGCTTAAATTTTAAATATACATCAATTAACAGCGGTATCGCGTAGAGTT 1680
Qy 1681 CGTTATGCTGCTTCTCAACAAATGCTCTGAGGGTAACTGTGCGAGGGAGTACTACTTTT 1740
Db 1681 CGTTATGCTGCTTCTCAACAAATGCTCTGAGGGTAACTGTGCGAGGGAGTACTACTTTT 1740
Qy 1741 GATCAAGGATTCCTCTAGTACTATGATGCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
Db 1741 GATCAAGGATTCCTCTAGTACTATGATGCAAAATGAGTCTTTGACATCTCAATCATTTAGA 1800
Qy 1801 TTTGCAAGATTTTCTGTAGGTAATAGTGCACTGCGAGGTCAAACTGCTGGAAATAGTATA 1860
Db 1801 TTTGCAAGATTTTCTGTAGGTAATAGTGCACTGCGAGGTCAAACTGCTGGAAATAGTATA 1860
Qy 1861 AGTAATATGCAAGTATGACAAACGTTTCACTTTGATAAATTTGAATTCATTCCCAATTACT 1920
Db 1861 AGTAATATGCAAGTATGACAAACGTTTCACTTTGATAAATTTGAATTCATTCCCAATTACT 1920
Qy 1921 GCAACCTTCGAAGCAGAAATACGATTTAGAAAGGGCGCAAGAGCGGTGAAATGCTCTGTTT 1980
Db 1921 GCAACCTTCGAAGCAGAAATACGATTTAGAAAGGGCGCAAGAGCGGTGAAATGCTCTGTTT 1980
Qy 1981 ACTAATACGAATCCCAAGAGATTGAAAACAGATGTGACAGATTTATCATATTGATCAAGTA 2040
Db 1981 ACTAATACGAATCCCAAGAGATTGAAAACAGATGTGACAGATTTATCATATTGATCAAGTA 2040
Qy 2041 TCCAAATTTAGTGGCGTGTATCGGATGAAATTCGCTTTAGATGAAAAGAGAAATTAATT 2100
Db 2041 TCCAAATTTAGTGGCGTGTATCGGATGAAATTCGCTTTAGATGAAAAGAGAAATTAATT 2100
Qy 2101 GAGAAAGTGAATATGCGAAACGACTCAGTGAAGAAAGAACTTACTCCAAGATCCAAC 2160
Db 2101 GAGAAAGTGAATATGCGAAACGACTCAGTGAAGAAAGAACTTACTCCAAGATCCAAC 2160
Qy 2161 TTCATCATCAATCAACGACCAAGCTTCAATCTACTATGAGCAATCGAATTTTCA 2220
Db 2161 TTCATCATCAATCAACGACCAAGCTTCAATCTACTATGAGCAATCGAATTTTCA 2220
Qy 2221 TCTATCCATGAACCAATCTGAACAGTGTGGGAGTGAAGACATTAATCCAGGAA 2280
Db 2221 TCTATCCATGAACCAATCTGAACAGTGTGGGAGTGAAGACATTAATCCAGGAA 2280
Qy 2281 GGAATGAGCTATTTAAAGAGATTAAGTCACTACCGGGGACTTTTAAATGAGTGTAT 2340
Db 2281 GGAATGAGCTATTTAAAGAGATTAAGTCACTACCGGGGACTTTTAAATGAGTGTAT 2340

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QY 2341 CCGACGATTTATATCAAAAAATAGGAGTCGGAATTTAAAGCTTATATCTCGTCAACAA 2400
Db 2341 CCGACGATTTATATCAAAAAATAGGAGTCGGAATTTAAAGCTTATATCTCGTCAACAA 2400
QY 2401 TTAAGAGGTTATTTAGAGATAGTCAGATTTAGAGATATATTTGATTCGTTTAAATGCG 2460
Db 2401 TTAAGAGGTTATTTAGAGATAGTCAGATTTAGAGATATATTTGATTCGTTTAAATGCG 2460
QY 2461 AAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGATGCGCGCTTTCAGTTGAAAGC 2520
Db 2461 AAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGATGCGCGCTTTCAGTTGAAAGC 2520
QY 2521 CCAATCGAAGGTCGGAGAACCGAATCGATGCGCACACATTTTGAATGAAATCCCTGAT 2580
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Db 2581 CTAGATTTCTTCGAGAGATGGAAGAAATGTCGGCATCATTTCCCATCATTTCTCTTTG 2640
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Db 2641 GATATTGATATTGATGCAAGATCTTGATGAGATCTAGGCGTGTGGTGGTATTCAAG 2700
QY 2701 ATTAAGACCGAGGATGTCAGAGACTAGGGAATCTGGAATTTATTTGAAGAAACCA 2760
Db 2701 ATTAAGACCGAGGATGTCAGAGACTAGGGAATCTGGAATTTATTTGAAGAAACCA 2760
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QY 2821 GAAAACTTACAAATTTGGAACCAAAACGAGTATATACAGAGGCAAAAGAGCTGTCGATGCT 2880
Db 2821 GAAAACTTACAAATTTGGAACCAAAACGAGTATATACAGAGGCAAAAGAGCTGTCGATGCT 2880
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Db 2881 TTATTGATGATCTCAATATAATAGATTTACAAGCGGATACAAACATTTGGCATGATTCAT 2940
QY 2941 GCGGAGATTAACCTGTTTCATCGAATTCGAGAGCTTATCTGTCAGATTTATCTGTTATC 3000
Db 2941 GCGGAGATTAACCTGTTTCATCGAATTCGAGAGCTTATCTGTCAGATTTATCTGTTATC 3000
QY 3001 CCGGTTGTAATGCGGAAATTTTGAAGATTTAGAGGTCGCAATTTACCTGCAATCTCC 3060
Db 3001 CCGGTTGTAATGCGGAAATTTTGAAGATTTAGAGGTCGCAATTTACCTGCAATCTCC 3060
QY 3061 CTATACGATCGAGAAATGTCGTTAAAAATGCTGATTTTAAATATGATTTAGCATGCTGG 3120
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QY 3121 AATGTAAGGGCATGTAGATGTACAAGAGCCATCACCGTCTGTCCTGTTGTTATCCCA 3180
Db 3121 AATGTAAGGGCATGTAGATGTACAAGAGCCATCACCGTCTGTCCTGTTGTTATCCCA 3180
QY 3181 GAATGGAAGCAGAAAGTGTCAAGAGCTGTCGCGTCTGTCGCGGCGTGGCTATATCTCTC 3240
Db 3181 GAATGGAAGCAGAAAGTGTCAAGAGCTGTCGCGTCTGTCGCGGCGTGGCTATATCTCTC 3240
QY 3241 CGTGTCAAGCGTACAAGAGGGATATGAGAGGGTGTGTGTAACGATCCATGAAATCGAG 3300
Db 3241 CGTGTCAAGCGTACAAGAGGGATATGAGAGGGTGTGTGTAACGATCCATGAAATCGAG 3300
QY 3301 AACATACAGACGAACTTAAAACTGTGTAAGAGAGGAGTGTATCCAACCGAT 3360
Db 3301 AACATACAGACGAACTTAAAACTGTGTAAGAGAGGAGTGTATCCAACCGAT 3360
QY 3361 ACAGGAAGCTGTATGATTTACTGCAACCAAGGTAACAGAGTGTGTAATTCCTCGGTAAT 3420
Db 3361 ACAGGAAGCTGTATGATTTACTGCAACCAAGGTAACAGAGTGTGTAATTCCTCGGTAAT 3420
QY 3421 GCTGGATATGAGGATGCAATGAAAGTTGATATACAGCATCTGTTAAATTAACAAACCGACT 3480
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Db 3421 GCTGGATATGAGGATGCAATGAAAGTTGATATACAGCATCTGTTAAATTAACAAACCGACT 3480
QY 3481 TATCAAGAGAAAGCTATACAGATGTACGAGAGATCAATCTGTAATATGACAGAGG 3540
Db 3481 TATCAAGAGAAAGCTATACAGATGTACGAGAGATCAATCTGTAATATGACAGAGG 3540
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QY 3601 GAAACCGATTAAGTATGATTTGAGATTTGAGAAACGGAAGGAAATTTATTTGTAAGAC 3660
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Db 3661 ATAGAAATTAATCTCTTATGAGAGGATAG 3687

RESULT 3
US-10-428-961-62
; Sequence 62, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MSCO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-428-961-62

Query Match      88.4%; Score 3260.2; DB 15; Length 3684;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 3445; Conservative 0; Mismatches 233; Indels 15; Gaps 3;

QY 1 TTGACTTCAATAGGAAAAATGAGAAATTAATAATGCTTTATCGATTCCAGCTGTA 60
Db 1 TTGACTTCAATAGGAAAAATGAGAAATTAATAATGCTTTATCGATTCCAGCTGTA 60
QY 61 TCGAATCATTTCCACACAAATGGATCTATCACAGATGCTCGTATTTAGGAGTCTTTGGT 120
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RESULT 4
US-10-809-953-9
; Sequence 9, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joss, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTI
; TITLE OF INVENTION: CRYSTAL PROTEINS
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; PRIORITY FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/661,016
; PRIOR FILING DATE: 2000-09-13
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; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 3687
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-10-809-953-9

Query Match 85.0%; Score 3133.6; DB 17; Length 3687;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 3373; Conservative 0; Mismatches 299; Indels 30; Gaps 3;

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Qy 1376 AACGACCAAAATTATGAATCATATAGTCAATAGTTTATCTACATAGGGCTCATTTCACAAT 1435
Db 1373 AGAGACCAAACTACGAGTCTTACTCTCATAGACTTCTTAACATTCGTTGAATCTCTGGAA 1432
Qy 1436 CTAGGGTGCAATGATCACAGTATATCTTTGGACGACCGGTAGTCAGATCGTCAAAATACCA 1495
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Qy 1496 TTAGTTTCAGATAGCATAAACAATAACCACTTGTGAATTAATCATTTCAACCTTATTCAGGTA 1555
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Qy 1556 CTTCTGTAGTCACTGGGCCAGGATTTACAGGAGGGGATATAATCCGAACTAAAGTTTAAATG 1615
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RESULT 6
US-09-988-462-6
; Sequence 6, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
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; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
;
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
;
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/988 462
; FILING DATE: 20-No. US20030046726A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/547,422
; FILING DATE: 11-APR-2000
; APPLICATION NUMBER: US 08/459,504
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3621
; OTHER INFORMATION: /product= "Full-length, maize
; optimized cryiB"
; /note= "Disclosed in Figure 6."
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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; US-09-988-462-6
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Query Match 40.6%; Score 1495.6; DB 10; Length 3624;
Best Local Similarity 63.7%; Pred. No. 0;
Matches 2310; Conservative 0; Mismatches 1299; Indels 15; Gaps 2;

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QY 139 ATCAATCCACTTGTAGCGCATCAACAGTCAACACGGGTATTACATAGCTGTGTAGATA 198
Db 61 ATCGACCCCTTGTGAGCGCCAGCACCGTGCAGACCGCATCAACATCGCGCGCGCATC 120
QY 199 CTAGGTGTATTAGCGGTACCGTTTGTGCGGACAAATAGCTAGTTTATTAGTTTCTGTT 258
Db 121 CTGGCGTGTGGCGGTGCGCTTTCGCGCGCAGCTGCGCCAGCTTCTACAGCTTCTCGTG 180
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Db	301	CTGGCGCAGACTTCCGCGCCTTACCAGCAGAGCCTGGAGGACTGGCTGGAGAACCGCGAC	360
Qy	439	GATCAAGAACGAGAGTGTCTTTATACCNAATATATAGCCTTAGAATCTTGATTTTCTT	498
Db	361	GACGCCCGCAACCGCAGCGTGTGTACACCCAGTACATCGCCCTGGAGCTGGACTTCCTG	420
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Db	421	AACGCCATGCCCTGTTCCGCATCCGCAACCAAGAGGTGCCCTGCTGATGGTGTACGCC	480
Qy	559	CAAGCTGCAATTTACACCTATTATTATGAGAGATGCCTCTCTTTTGGTAGTGAATTT	618
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Db	781	CTGACCGCGAGGTGTACCGACGCCATCGCGCGCACCGCGGTGAACATGGCCAGCATG	840
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Qy	1279	ACTTTTGAAGAGTACTGCTACTATAGTCAACCTCATAGTCACTGGGCTTCAATTA	1338
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Db 2401 GACGTGCCGCGACCGAGGCTGTGGCCCTTGAGCGTGGAGAGCCCATCGGCCGCTGC 2460
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RESULT 7

US-09-826-660-5
; Sequence 5, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; CURRENT APPLICATION NUMBER: US/09/826,660
; FILE REFERENCE: MA-714XC2D1
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3522
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-826-660-5

Query Match 38.2%; Score 1408.4; DB 9; Length 3522;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1061; Indels 108; Gaps 9;

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Db 807 AGTAATTTGAGGATCTCCAGTTTCG-----TAATATACCTTAA 845
Qy 945 GTTTTCCGCTATAGAGATCGGGTTATCCGAAGCCCGCATCTACTGTATTTCTTAGAACA 1004
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Qy 1005 ACTTACAATTTTAGCACTTCTACGATGAGTGTCTACTAGGATATGACTTACTGGCG 1064
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Qy 1065 GGGGCACACAATTCATCTCGGCCAAATAGGAGGGGGATTAATACCTCAACGCAATGGTTC 1124
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Qy 1185 TGAATCATATACGAGAGTCTTCTATGGGGAATTTACCTTGAACCTATTCTATGGTGTCCC 1244
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Qy 1245 TACTGTTAGATTTAATTTTAGGAACCTCAGAAATPACTTTTGAAGAGGTACTGCTAACTA 1304
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Db 2071 -----CGTGGTTGAGAGGAAGTAC 2090
Qy 2262 GAACTATCAATTCAGAGGAAGAAATGAGCTATTTAAAGAGAAATACGTCACTACCGGG 2321
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Qy 1305 TAGTCAACCTATAGTACCTGGCTTCAATTAAGAAATTCAGAAATCTGAATTTACCAAC 1364
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Qy 2202 TGAGCAATCGAATTTTCACTATCTATCCATGAACAACTCTGAACATGGATGGTGGGAAGTGA 2261
Db 2071 -----CGTGGTTGGAGAGAGTAC 2090
Qy 2262 GAACATTACATCCAGAGAGAAATGACGTATTTAAAGAGAAATTAAGTCACTACCGGG 2321
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Db 2071 -----CGTGGTGGAGAGGAAGTAC 2090
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Db 2871 TATTTTCACTGCAATCTCTTATATGATGCGAGAAATGTCATTTAAATACCGTGATTTCAA 2930
Qy 3102 TAATGGATAGCATGCTGGAATGTAAAGGCGATGTAGATGT---ACAACAGAGCCATCA 3158
Db 2931 TAATGGCTTATCATGCTGGAACGTTGAAAGGCGATGTAGATGTAGAGAAACAAACCA 2990
Qy 3159 CCGTTCTGCTCTGTTATCCAGAAATGGAAGAGAGAGTGTCAACAAGCAGTTCGGCTG 3218
Db 2991 CCGTTCTGCTCTGTTGTTCCGGAATGGAGAGAGAGTGTCAACAAGAGTTCGTGCTG 3050
Qy 3219 TCCGGGGCGTGGCTATATCTCTCGTGTACAGCGGTACAAAGAGGGATATGAGAGCGGTTG 3278
Db 3051 TCCGGGTGCTGGCTATATCTCTCGTGTACAGCGGTACAAAGGAGGATATGGAGAGGTTG 3110
Qy 3279 TGTAAACGATCCATGAAATCGAGAACATACAGCGAACTAAATTTTAAATCTGTGAAGA 3338
Db 3111 CGTAAACATTCATGAGATCGAGAACATACAGCGAACTGAAGTTTATAGCAACTGCGTAGA 3170
Qy 3339 AGAGGAAGTGTATCCAAACGATACAGGAACGTTGTATGATTTATCTGCAACCAAGGTAC 3398
Db 3171 AGAGGAAGTGTATCCAAACCAACCGGTAAACGTTGATTTATCTGCAATCAAGAA 3230
Qy 3399 A-----GCAGTATGTAAATTTCCCGTAAATGCTGGAATGAGGATGCAATGAAATGATAC 3452
Db 3231 ATACGGGGGTGCGTACACTTTCCCGTAAATCGTGGATATGACGAAACCTTATGGAAGCAATTC 3290
Qy 3453 TACAGCATCTGTTAAATTTACAAACCGACTTATGAAGAGAAACCGTATACAGATCTACGAG 3512
Db 3291 TTCTGTACCAAGCTGATTTATGCGTCACTTATGAAGAAATATCGTATACAGATGGAGGAAG 3350
Qy 3513 AGATATCATTTGTAATATGACAGAGGATGTGGAATTTATCCACCACTACCACTCGGTGTTA 3572
Db 3351 AGACAATCTTTGTAATTAACAGAGGATATGCGGATTTACACCACTACCACTCGGTGTTA 3410
Qy 3573 TATGACAAAGAAATTAAGAAATCTTCCAGAAACCGAATAAGGTATGATTTGAGATTGGAGA 3632
Db 3411 TGTGACAAAGAAATTAGAGTACTTCCAGAAACCGGATAGGTATGGATTGAGATCGGAGA 3470

QY 3633 AACGGAAGGAAGTTTATTGTAGACAGCGTGGAAATTAATCTTATGGAGAA 3684
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Db 3471 AACGGAAGGAACATTCATCGTGACAGCGTGGAAATTAATCTTATGGAGAA 3522
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RESULT 10

US-09-873-873-25
; Sequence 25, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; FILE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-09-873-873-25

Query Match 38.0%; Score 1402; DB 9; Length 3534;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

QY 285 TCAGTGGGAATTTCTTAGACATGTCGAACAATTAATAATCAACAATAACAGAA 344
|||||
Db 213 TCATGGGAGCGATTTCTGTACAAATGGAACAGTTAATACCAAGAAATGAAGAATT 272
|||||
QY 345 TGCTAGGAATACGGCACTTGCTCGAATTAACAAGTTTAGAGATTCTTTAGAGCCATCA 404
|||||
Db 273 CGCTAGGAACCAAGCCATTTCTAGATTAGAGCACTAGCAATCTTATCAATTTACGC 332
|||||
QY 405 ACAGTCACCTTGAAGATTGCTTAGAATAACCGTGATGATGACGAAGACGAGATGTTCTTTA 464
|||||
Db 333 AGAATCTTTTAGAGAGTGGGAAGCAGATCTCTACTAATCCAGCATTTAAGAGAAGAGATGCG 392
|||||
QY 465 TACCCAATATATAGCCTTAGACTTGAATTTCTTAATGCGATGCCGCTTTTCGCAATTAG 524
|||||
Db 393 TATTCATTTCAATGACATGAACAGTGCCCTTACAAACCGCTATCTCTTTTTCGAGTTCA 452
|||||
QY 525 AAACCAAGAAGTTCCATTTAATGGTATATCTCAAGCTGCATAATTTACACCTATTATT 584
|||||
Db 453 AAATTTATCAAGTTCTCTTTTATCAGTATATGTTCAAGCTGCATAATTTACATTTATCAGT 512
|||||
QY 585 ATTGAGAGATGCTCTCTTTTGGTAGTGAATTTGGGCTTACATCGCAGGAATTTCAACG 644
|||||
Db 513 TTTGAGAGATGTTTCAGTGTTTGGACAAAGGTGGGGAATTTGATGCCGCACTATCAATAG 572
|||||
QY 645 TTATTTATGAGCCCAAGTGGACAAACAGAGATTATTCGACTATTGCTAGATGTA 704
|||||
Db 573 TCGTTATATGATTTAACTAGGCTTTATTGGCAACTATACAGATCATGCTGACGCTGTA 632
|||||
QY 705 TAATACAGCTCTAAATAGCTTTCAGAGGAGCAAAATCCGCAAGTTGGGTGCGTTAATAATCA 764
|||||
Db 633 CAATACGGGATTAGACGCTGTTATGGGACCGGATTTCTAGAGATTGGATAAGATATAATCA 692
|||||
QY 765 ATTCGCTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCATTATTTCCCAAGCTATGA 824
|||||

Db 693 ATTTAGAGAGAAATTAACAATACTGTATTAGATATCGTTCTCTATTTCGAACTATGA 752
QY 825 CACTCGCACTTATCCAAATAAATAGAGTGTCTCAGTTAAACAAGGGAAGTTTATACAGAGC 884
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Db 753 TAGTAGAACGATTCCAATTCGAAACAGTTTCCCAATTAACAAGAGAAATTTATACAAACC 812
|||||
QY 885 A--ATTGGAGCAACAGGGGTAAATATGCAAGTATGAATTGGTATAATAATAATGCACCT 942
|||||
Db 813 AGTATTAGAAAAATTTTGTATGTAGTTTTCGAGGCTCGGCTCAGGSCATAGAAAGAAGTAT 872
|||||
QY 943 TCGTTTCCGCTATAGAGACTGCGGTATCGAAGCCCGCATCTACTACTTGTATTTCTTAGAA 1002
|||||
Db 873 TAGGAGTCCACATTTGATGGATATACCTTAAACAGTATAACCATCTATACGGATGCTCATAG 932
|||||
QY 1003 CAACCTTACAAATTTTAGCACTTCAACAGATGGAGTGTCTACTAGSCATATGACTTACTGG 1062
|||||
Db 933 GGGTTATTATTATGTGTCAGGGCATCA-----AATAATGGCTTCTCTGTAGGGTT 983
|||||
QY 1063 CGGGGGCAACAATTCATCTCGGCCAATAGAGCGGATTTAAATPACCTCAACGATGGG 1122
|||||
Db 984 TTCGGGGCCAGAAATTCACCTTTCCGCTATATGGAACATATGGGA-----ATGCA 1032
|||||
QY 1123 TCTACCAATACTCTTATTAATCCTGTAAAGATTAATCTCTCTCTCGAGACGTATATTGG 1182
|||||
Db 1033 GCTCCACAACAACGATTTGTTGCTCAACTAGGTCAAGGCGGTATAGAACATTTATCGTCC 1092
|||||
QY 1183 ACTGAATCATATGAGGAGTGTCTTATGCGGAATTTACCTTGAACCTATTTCATGGTCTC 1242
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Db 1093 ACTTATATAGAACACCTTTTAAATATAGGGAATAATAATCAACAACATCTCTGTTCTTGAC 1152
|||||
QY 1243 CCTACTGTTAGATTTAAATTTAGGAACCTCAGAAATCTCTTTTGAAGAGGTACTCTTAAC 1302
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Db 1153 GGGAC---AGAATTTGCTTATGGAACCTCTCTCAAAATTTGCCATCCGCTGTATACAGAA 1208
|||||
QY 1303 TATAGTCAACCTATAGTCACTCGGCTTCAATTTAAAGATTCAGAACTG-AAATTACC 1361
|||||
Db 1209 AAGCGGAACGATAGTTCGCTGGATGAATACCGCCACAGAAATCAACAGTGCACCTAG 1268
|||||
QY 1362 ACCAGAACACACAGACGACCAAAATTAATGATCATATAGTATAGTTTATCTCACATAGG 1421
|||||
Db 1269 GCAAGGATTTAGTCATCGATTTAAGCCATGTTTCAATGTTTCGT-----CAGGCTTTAG 1322
|||||
QY 1422 GCTCATTTTCAAACTCTAGGGTGCATGTACCAAGTATATTTCTTGGAGCGCACCGTAGTGCAGA 1481
|||||
Db 1323 TAATAGTAGTGTAAATTAAGAGCTCCAAATGTTTCTTGGAGCGCACCGTAGTGCAC 1382
|||||
QY 1482 TCGTACAAATACCAATTTAGTTCAGATAGCAATAACAATACATTTGGTAAATCAATCAA 1541
|||||
Db 1383 CCTACAAATACAATTTGATCCGAGAGGATTTACTCAAAATACCATTTGGTAAAGCACATAC 1442
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QY 1542 CCTTAATTCAGGTACCTCTGTAGTCCAGTGGCCAGGATTTTACAGAGGGGATATAATCCG 1601
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Db 1443 ACTTCAGTCAAGTACTCTGTGTGAAGGCGCCGGGTTTACGGAGAGGATATTTCTTCG 1502
|||||
QY 1602 AACTAAGCTTAATGGTATGTACTAAGTATGGGTCTTTAAATTTTAAATAATCAATTTACA 1661
|||||
Db 1503 ACGAAACAGTGGAGGACCATTTGCTTACTATTTGTTTAAATAATAATGGCAATTTACCCCA 1562
|||||
QY 1662 GCGGTATCGGTGAGAGTTCGTTATGCTGTTCTCAAAACAATGGTCTCGAGGGTAACTGT 1721
|||||
Db 1563 AAGGTATCTGTCAAGAAATACGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACCGT 1622
|||||
QY 1722 CGGAGGAGTACTACTTTTGTATCAAGGATTCCTTAGTACTATGATGTCAAATGATGCTTT 1781
|||||
Db 1623 TGCAGGTGAACGGAATTTTGTGCTGCTCAATTTAAACAAACAAATGGATACCGGTGACCCAT 1682
|||||
QY 1782 GACATCTCAATCAATTTAGATTTGAGAAATTTCTGTAGGTATTAGTGCATCTGGCAGTCA 1841
|||||
Db 1683 AACATTCATCTTTTAGTTACGCACTTATTAATACAGCTTTTACATTTCCCAATGAGCCA 1742
|||||
QY 1842 AACTGCT---GGAAATAGTATAGTAAATATGAGGTAGACAAACGTTTCTCTTTGATAA 1898
|||||
Db 1743 GAGTAGTTTTCACAGTAGTGTGCTGATCTTTTGTAGTTTCAGGGAATGAAGTTTATATAGACAG 1802
|||||

1899 AATTGAATTCATTCCAAATTAAGTCAACCTTCGAGCAGAAATACGATTTAGAAAGGCGCA 1958
1803 ATTTGAATTTGATTCAGTTACTGCAACATTTGAAGCAGAAATATGATTTAGAAAGACACA 1862
1959 AGAGCGGTGAATCTCTGTTTACTAATACGAATCCAGAAAGATTTGAAACAGATGTGAC 2018
1863 AAAGCGGTGAATGCGGTGTTTACTTCTAATACCAGATAGGAGATAAAAACAGATGTGAC 1922
2019 AGATTATCATATTGATCAAGATATCCAAATTTAGTGGGTGTTTATCGGATGAATTTCTGCTT 2078
1923 GGATTAATCATATTGATCAAGATATCCAAATTTAGTGGATTTGTTATCAGATGAATTTGCTT 1982
2079 AGATGAAGAGAGAGAATTTACTTCGAAAGTGAATATGAGAAACGACTCAGTGATGAAG 2138
1983 GGATGAAGAGAGAGAATTTGTCGAGAAAGTCAAAACATGCGAAGCACTCAGTGATGAGCG 2042
2139 AAATTTACTCCAAAGATCCAAACTTCCATCCATCAATAGCAACAGCACTTCATATCTAC 2198
2043 GAATTTACTTCAAGATCCAAACTTCAAGGCATCAATAGGCATCTAGAC----- 2091
2199 TAATGAGCAATCGAATTTACATCTATCCATGCAATCTGAACATGATGATGGTGGGAG 2258
2092 -----CGTGGTTGGAGGAG 2108
2259 TGAGAAATTTACAAATCCAGAAAGGAAATGACGATTTTAAAGAGAAATACGTCACACTACC 2318
2109 TAGCGATATACCATCCAAAGAGGAGATGACGATTTTCAAGAAATTTATGTCACACTACC 2168
2319 GGGGACCTTTAATGATGTTATCCGACGATTTTATATCAAAAAATPAGGAGAGTCGGAAT 2378
2169 AGGTACCTTTGATGATGTTATCCAAACATATTTGTTATCAAAAAATCGATGAATCAAAAT 2228
2379 AAAAGCTTTACTCGCTACCAATTAAGAGGATATATGAAGATAGTCAAGATTTAGAGAT 2438
2229 AAAAGCTTTACCGCTTATCAATTAAGAGGATATATGAAGATAGTCAAGATTTAGAAAT 2288
2439 ATATTGATTCGTTAATGCGAAACATGAAACATTTGATTTCCAGGTACCGAGTCCGT 2498
2289 CTATTAAATTCGCTACAAATGCAAAACATGAAACAGTAAATGTGCGACGTACGGGTTCTT 2348
2499 ATGGCGGCTTTCAAGTTGAAGCCCAATCGGAAGTGGGAGAACCGAATCGATCGGACC 2558
2349 ATGGCGGCTTTCAAGCCCAATCGCAATCGGAAGTGGGAGAACCGAATCGATCGGACC 2408
2559 ACATTTGAATGGAATCTCGATCTAGATTTCTCGCAGAGATGGAGAAATGTCGCA 2618
2409 ACACCTTGAATGGAATCTCGATCTAGATTTCTCGCAGAGATGGAGAAATGTCGCA 2468
2619 TCATTCCCATCATTTCTTTGGATATTTGATTTGATGTCACAGATTTGATGATGAGAAATCT 2678
2469 TCATTCCCATCATTTCTTTGGATATTTGATTTGATGTCACAGATTTGATGATGAGAAATCT 2528
2679 AGGCGTGGGTGATTTCAAGATTTAAGACGAGGAGGTCATGCAAGACTAGGGAATCT 2738
2529 AGGTGATGGGTGATCTTTAAGATTTAAGACGCAAGATGGCAGCAAGACTAGGGAATCT 2588
2739 GGAATTTATTGAAGAGAACCATTTATAGAGAACGACTGTCTGCTGTAAGAGAGCAGA 2798
2589 AGATTTCTCGAAGAGAACCATTTAGTAGAGAGCGCTAGCTGCTGTTGAAAGAGCGCA 2648
2799 GAAAAATGAGAGACAAACGTTGAAAACTTACAAATTTGGAATGGAACAAATATCGTTTAAAGA 2708
2649 GAAAAATGAGAGACAAACGTTGAAAACTTACAAATTTGGAATGGAACAAATATCGTTTAAAGA 2708
2859 GGCAGAGAGCTGTGATGCTTTTATTTGATTTCTCAATATAATAGATTACAAGCGCA 2918
2709 GGCAGAGAGCTGTGATGCTTTTATTTGTAACCTCTCAATATGATCAATTACAGCGCA 2768
2919 TACAAACATTTGGCATGATTCATGCGGCAGATAAACTTTGTTTCAATCGAATTCGAGGCTTA 2978
2769 TACGAATATTGCCATGATTCATGCGGCAGATAAACTTTGTTTCAATCGAATTCGAGGCTTA 2828

2979 TCTGTCAGAATTTATCTGTATTCGGGTGTAATAATGCGGAAATTTTGAAGAAATTAGAAG 3038
2829 TCTGCTGAGCTGTCTGTGATTCGGGTGTCAATGCGGCTATTTTGAAGAAATTAGAAG 2888
3039 TCGCATTTATCAGTCAATCTCCCTATACGATGCGAGAAATGTCTGTTAAATAATGGTGAAT 3098
2889 GCGTATTTTCTAGTCAATCTCCCTATATGATGCGAGAAATGTCTTAAATAATGGTGAAT 2948
3099 TAATAATGGAATAGCATGCTGGAATGTAAAGGGCATGTAGATGT--ACAACAGAGCCA 3155
2949 TAATAATGGCTTATCTCTGCTGGAACGTGAAAGGCGATGTAGATGTAGAGAAACAA 3008
3156 TCACCGTTCTGCTGCTGTTATCCAGATGCGAGAGCAGAGTGTCAACAGAGTTCGCT 3215
3009 CCAACGTTCTGCTGCTGTTTCCGGAATGGGAAGCAGAGTGTCAACAGAGTTCGCT 3068
3216 CTGTCGGGGCTGGCTATATCTCCGTCGTACAGCGTCAAAAGAGGGATATGGAGGG 3275
3069 CTGTCGGGGCTGGCTATATCTCTGCTCACAGGCTACAGGAGGATATGGAGAGG 3128
3276 TTGCTGAACGATCCATGAAATCGAGAAATACAGAGCAATACAGAGCAATCTGCA 3335
3129 TTGCTGAACGATCCATGAAATCGAGAAATACAGAGCAATCTGCA 3188
3336 AGAAGAGGAGTGTATCCCAACGATACAGAAACGAACTTAAATAATTTAAATACTGTGA 3395
3189 AGAAGAGGAGTGTATCCCAACGATACAGAAACGAACTTAAATAATTTAAATACTGTGA 3248
3396 TACAGCGATGTATTAATTCGCTGATGCTGATGATGATGATGATGATGATGATGATGAT 3455
3249 AGAATACGAGGCTGGCT-----ACACTTCTCGTAATCGAGGATATAACGAAGCTCTTC 3302
3456 AGCATCTGTTAATTAACAAACGACTTATGAAGAGAGAGAGGATACAGATGTACGAGAGA 3515
3303 CGTACAGCTGATTTATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 3362
3516 TAATCATTTGTGAATATGACAGAGGATGTGAATTTATCCACCTACCAGCTGTTATAT 3575
3363 GAATCTTTGTGAATTTAAGAGAGGATATAGGATTTACAGGCTACCTACAGCTGTTATAT 3422
3576 GACAAAGAAATTTAGAAATCTTCCAGAGAGGATATAGGATTTACAGGCTACCTACAGCT 3635
3423 GACAAAGAAATTTAGAAATCTTCCAGAGAGGATATAGGATTTACAGGCTACCTACAGCT 3482
3636 GGAAGGAGGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3687
3483 GGAAGGAGGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3534

RESULT 11

US-09-916-956A-25

; Sequence 25, Application US/09916956A

; Publication No. US20030017571A1

; GENERAL INFORMATION:

; APPLICANT: Malvar, Thomas

; APPLICANT: Gilmer, Amy Jelen

; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins

; FILE REFERENCE: WCO/2111--1

; CURRENT APPLICATION NUMBER: US/09/916,956A

; PRIOR APPLICATION NUMBER: US 09/253,331

; PRIOR FILING DATE: 1999-02-19

; PRIOR FILING DATE: 1997-09-03

; PRIOR APPLICATION NUMBER: US 08/922,505

; PRIOR FILING DATE: 1996-11-20

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 25

; LENGTH: 3534

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

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; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-09-916-956A-25

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Query Match 38.0%; Score 1402; DB 10; Length 3534;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

QY	1243	CCTACTGTTAGATTTAAATTTTATAGAAACCCCTCAGAAATATCTTTTGAAGAGGTACTGCTAAC	1301
DB	1153	GGGAC-----AGAATTTGCTTATGGAACCTCTCAAAATTTGCCATCGCTCTATACAGAAA	1208
QY	1303	TATAGTCAACCCATAGAGTCACCTGGGCTTCAATTAAGATTCAGAAAATG-ANTTACC	1361
DB	1209	AAGCGGAACGGTAGATTTCGCTGGAGTAAATACCGCCACAGAAATAACACGTCGCCACTAG	1268
QY	1362	ACCAGAAACACAGAAACGACCAAAATATGAATCATATAGTCATAGGTTATCTCACATAGG	1421
DB	1269	GCAAGGATTAGTCATCGATTAGCCCATGTTCAAATGTTTCGT-----TCAGGCTTTAG	1322
QY	1422	GCTCATTTACAATCTTAGGGTGCATGTACAGATATATCTTTGGACGACCGTAGTGCAGA	1481
DB	1323	TAATAGTAGTGTAAAGAGCTCCAAATGTTTTCTTTGGACGCACCGTAGTGCAC	1382
QY	1482	TCGTACAAAATACCAATTAGTTTCAGATAGCATAAACACAAATACCAATCGTAAATCANTTCAA	1541
DB	1383	CCCTACAAATACCAATTGATCCGAGAGGATTACTCAAAATACCAATGGTAAAGCACAATAC	1442
QY	1542	CCTTAATTCAGGTACCTCTCTAGTCAGTGGCCCGCAGGATTTACAGGAGGGGATATAATCCG	1601
DB	1443	ACTTCAGTCAGTACTACTCTGTTAGAGGGCCCGGGTTTACGGGAGGAGATATCTTCG	1502
QY	1602	AACTAACGTTAAATGGTAGTGTACTAAAGTATGGGTCTTAAATTTTAAATAATCATCATTTACA	1661
DB	1503	ACGAAACAATGGGAGGACCAATTCGTTTATACTATTTGTTAATATAAATGGGCAATTAACCCCA	1562
QY	1662	CGGGTATCGCGTGAGAGTTCGGTTATGCTGCTTCTCAAAACATGGTCTGAGGGTAACTGT	1721
DB	1563	AAGGTATCGTGCAGGAATACGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACGGT	1622
QY	1722	CGGAGGGAGTACTACTTTTCATCAAGGATTCCTAGTACTATGAGTGCATAACAGTCTTT	1781
DB	1623	TGCAGGTGAACGATTTTCTGCTGCTCAATTAACAAACATGATACCGTGACCAAT	1682
QY	1782	GACATCTCAATCAATTTAGATTTTCAGAAATTCCTGTAGGTATTAGTGCACTCGGCAGTCA	1841
DB	1683	AACATTCCAATCTTTTAGTTTACGCAACTTAATAACAGCTTTTACATCCCAATGAGCCA	1742
QY	1842	AACGTCT---GGAATAGTATAGTAATAATGCAGGTAGACAAACGTTTCACCTTTGATAA	1898
DB	1743	GAGTAGTTTCACAGTAGGTGCTGATCTTTTAGTTTACAGGGAATGAAGTTTATATAGACAG	1802
QY	1899	AAATTGAATTCATTTCCAAATTACTGCAACCTTCGAAGCAGAAATACGATTAGAAAGGGCGCA	1958
DB	1803	ATTTGAATTCGATTCAGATTCTGCAACATTTGAAGCAGAAATATGATTTAGAAAGACACA	1862
QY	1959	AGAGGGCGTGAATGCTCTGTTTACTAATACGAAATCCAAAGAAGATTGAAAACGATGTGAC	2018
DB	1863	AAAGGGCGTGAATGCGCTGTGTTACTTCTATAAACCAAAATAGGGATAAAAACAGATGTGAC	1922
QY	2019	AGATTATCATTTGATCAAGTATCCAAATTTAGTGGCGGTGTTATCCGATGAATTCGTCT	2078
DB	1923	GGATTATCATATTTGATCAAGTATCCAAATTTAGTGGGATTTGTTTATCAGATGAATTTTGTCT	1982
QY	2079	AGATGAAGACAGAGAATTACTTCAGAAAGTGAATATGCGAAACGACTCAGTGATCAAG	2138
DB	1983	GGATGAAGACGAGAATTTGTCGGAAGATGCAACATGCGAGCGGACTCAGTAGTAGGG	2042
QY	2139	AAACTTATCTCAAGATCCAAACTTCATCCATCAATAAGCAACCAAGACTTCATATCTAC	2198
DB	2043	GAATTTACTTCAAGATCCAAACTTCAAAGGCATCAATAGGCAACTAGC-----	2091
QY	2199	TAATGAGCAATCGAATTTTCACATCTATGCCATGAACAACTGGAACATGGATGGTGGGGAAG	2258
DB	2092	-----CGTGGTTGGAGAGGAAG	2108
QY	2259	TGAGACATTTACAATCCAGGAAGGAATGACGTATTTTAAAGAGAATTACGTCACTACC	2318
DB	2109	TACGGATATTACCATCCAAGAGGAGATGACGTATTTCAAGAAAAATTTATGTCACTACC	2168
QY	2319	GGGAGCTTTTAAATGAGTGTATCCGACGTATTTTATCAAAAAATAGGAGAGTCGGAAAT	2378

OTHER INFORMATION: Hybrid Delta-Endotoxin			
;	NAME/KEY: CDS	38.0%;	Score 1402; DB 10; Length 3534;
;	LOCATION: (1)...	Best Local Similarity 65.7%;	Pred. No. 0;
US-09-916-956A-25	LOCATION: (1)...	Matches 2243; Conservative 0;	Mismatches 1070; Indels 99; Gaps 10;
Qy	285	TCAGTGGGAATTTTCC	TAGAACATGTCGAACAACTTATAATCAACAATAACAGAAAA 344
Db	213	TCAATGGGCGCATTTCT	TGTACAAATTGAACAGTTAATTAAACAAAGATAGAGAATT 272
Qy	345	TGCTAGGAATACGGCACT	TGCTCCATTAACAGTTTAGGAGATTCTTTTAGAGCTATCA 404
Db	273	CGCTAGGAACCAAGCCATT	CTAGATTAGAGGACTAAGCAATCTTTATCAAAATTTAGCG 332
Qy	405	ACAGTCACTTGAAGATTGG	CTAGAAAAACCGTGATGATGCAAGAACGAGAGTGTCTTTTA 464
Db	333	AGAACTCTTTTAGAGATGG	GAACAGATCTTACTAATCCAGCATTAAGAGAGATGCG 392
Qy	465	TACCAATATATAGCCTTAG	AACCTTGAATTCGATGCGCTTTTCGCAATTAG 524
Db	393	TATTCAAATCAATGACAT	GAACAGTGCCTTACAACCGCTATTCTCTTTTGCAGTTCA 452
Qy	525	AAACCAAGAGTTCATATTA	TATGTTATATGCTCAAGCTGCATAATTTACACCTATTATT 584
Db	453	AAATATCAAGTTCCCTCT	TTTATCAGTATATGTTCAAGCTGCATAATTTACATTTATCAGT 512
Qy	585	ATTGAGAGATGCGCTCTCT	TTTGGTAGTAATTTGGGCTTACATCGCAGGAAATTTCAACG 644
Db	513	TTTGAGAGATGTTTCAGTG	TTTGGACAAAGGTGGGATTTGATGCCGCGACTATCAATAG 572
Qy	645	TTATATTAGCGCCAACTAG	CTGAGGAAACAAACGAGAGATTATTCGACTATTTCGCTAGAACTGTA 704
Db	573	TCGTTATAATGATTTAACT	AGGCTTATTGGCAACTATACAGATCATGCTGTACGCTGGTA 632
Qy	705	TAATACAGGTCTAAATAGCT	TGAGAGGACAAATGCGCAAGTTGGGTGGTTATATATCA 764
Db	633	CAATACGGGATTAGCGGTGA	TGGGACCGGATTTAGAGATTGGATAAGATATAATATCA 692
Qy	765	ATTCCGTPAGAGATCTAAAC	GTGTAGGGTATTAGATCTAGTGGCACAATTCCCAAGCTATGA 824
Db	693	ATTTAGAGAGAAATTAACAT	TAACCTGTTATTAGATATGTTTCTTATTTCCGAACTATGA 752
Qy	825	CACCTCGCATTTATCCAAATA	ATAGAGTGTCTAGTTAAACAGGGAAGTTTATACAGACGC 884
Db	753	TAGTAGAACGTATCCCAATTC	CGAAACAGTTTCCCAATTAAACAGAGAAATTTATACAAACCC 812
Qy	885	A--ATTGGAGCAACAGGGGT	AAATATGCGCAAGTATGAATTTGGTATATATATATATGCACT 942
Db	813	AGTATTAGAAAAATTTTGA	TGGTAGTTTTCAGGCTCGGCTCAGGGCATAGAAAGAGTAT 872
Qy	943	TCGTTTTCCGCTATPAGAC	ATGCGGTATTCCGAAGCCCGCATCTACTTTGATTTCTTAGAA 1002
Db	873	TAGGAGTCCACATTTGAT	GTGATATACAGTATTAACCATCTATACGGATGCTCATAG 932
Qy	1003	CAACTTACAATTTTATGAC	TTTCACTTCATACGATGAGTGTCTATAGGCATATGACTTACTGG 1062
Db	933	GGGTATTATTATTGGTTCAG	GGGATCA-----AATAATGGCTTCTCCTGTAGGGTT 983
Qy	1063	CGGGGGCACACAATTCAACT	CTCGGCCAATAGGCGGATTAATACCTCAACGCAATGGG 1122
Db	984	TTCGGGGCCAGAAATTTCACT	TTTCGGCTATATGNACTATGGGAA-----ATGCA 1032
Qy	1123	TCTACCAATATCTTCTTAAT	TCTGTGAAGATTATCATTTCTCTCGAGACGTATATTTGG 1182
Db	1033	GCTCCACAAACGATTTGTT	GTCTCACTAGTCAAGGCGGTGATAGAACATTTATCGTCC 1092
Qy	1183	ACTGAATCATATGACAGAG	TGCTTTATGGGGAATTTACCTTGAACCTATTCATGTTGTTGTC 1242
Db	1093	ACTTTATATAGAAGACCTTT	TAATATAGGGATAAATAACCAACATCTCTGTTCTTGAC 1152

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Db 2169 AGGTACCTTTGATGAGTGCTATCAACATATTTGTATCAAAAAATCGATGAATCAAAAT 2228
QY 2379 AAAAGCTTATCTCGCTACCAATTAAGAGGGTATATTGAAGATAGTCAAGATTTAGAGAT 2438
Db 2229 AAAAGCCTTTACCGCTTATCAATTAAGAGGGTATATCGAAGATAGTCAAGACTTTAGAAT 2288
QY 2439 ATATTTGATTCTGTTATATCGGAACATGAAACATTTGGATGTTCCAGGTACCGAGTCCGT 2498
Db 2289 CTATTTAAATTCGCTACATGCAAAACATGAACACAGTAAATGTGCCAGTACGGTTCCTT 2348
QY 2499 ATGGCCGCTTTCAGTTGAAGCCCAATCGGAAGGTGCGAGAACCGAATCGATCGCCACC 2558
Db 2349 ATGGCCGCTTTCAGCCCAAGTCCAATCGGAAGGTGCGAGAGCGAATCGATCGCGCC 2408
QY 2559 ACATTTTGAATGAATCCCTGATCTAGATTGTTCTGCGAGAGATGAGAAAAATGTGCGCA 2618
Db 2409 ACACCTTGAATGAATCCCTGATCTAGATTGTTCTGTTAGGGATGAGAAAAAGTGTGCCA 2468
QY 2619 TCATTCCTCAATTTCTCTTTGGATATTCATATTTGGATGCGAGACTTGCATGGAATCT 2678
Db 2469 TCATTCCTCAATTTCTCTTTAGACATTTGATGTAGATGTACAGACTTAAATGAGGACCT 2528
QY 2679 AGCGGTGCTGGTGTATTCGAATTAAGACGCGAAGGTCTATGCAAGCTAGGGAATCT 2738
Db 2529 AGGTGTATGGTGTATCTTTAAGATTAAAGACGCAAGATGGCGACGCAAGCTAGGGAATCT 2588
QY 2739 GGAATTTATTGAAGAGAACCAATTTATAGGAGACACTGTCTGTGTGAAGAGAGAGA 2798
Db 2589 AGAGTTTCTCGAAGAGAACCAATTTATAGGAGAGCGCTAGCTGTGTGAAGAGAGCGGA 2648
QY 2799 GAAAAATGAGAGACAAACGTTGAAAACTACAATTTGAAAAACAAACAGTATATACAGA 2858
Db 2649 GAAAAATGAGAGACAAACGTTGAAAAATTGGATGGGAACAAATATCTGTTTATAAGA 2708
QY 2859 GGCAAAAGAGCTGTGGATGCTTTATTTGTAGATCTCAATATATAGATTACAAGCGGA 2918
Db 2709 GGCAAAAGAGCTGTAGATGCTTTATTTGTAACTCTCAATATGATCAATTAAGCGGA 2768
QY 2919 TACAAACATTTGGCATGATTCATGCGGAGATAAACTTTGTCATCGAATTCGAGAGGCTTA 2978
Db 2769 TACGAATATTGCCATGATTCATGCGGAGATAAACTTTGTCATGCAATTCGAGAGGCTTA 2828
QY 2979 TCTGTCAGAATTAATCTGTTATCCCGGTGTAAATGCGGAATTTTGAAGAATTAGAAGG 3038
Db 2829 TCTGCTGAGCTGTGTGATTCGCGGTGTCAATGCGGCTATTTTGAAGAATTAGAAGG 2888
QY 3039 TCGCATTAATCACTGCAATCTCCCTATACGATGCGAGAAATGTCGTTAAATGCTGATTT 3098
Db 2889 CGGTATTTCACTGCAATCTCCCTATATGATGCGAGAAATGTCATTAATAATGCTGATTT 2948
QY 3099 TAATAATGGATTAGCATGCTGGAATGTAAAGGGCATGTAGATGT--ACAACAGAGCCA 3155
Db 2949 TAATAATGGCTTATCTGCTGGAACTGGAAGGGCATGTAGATGTAGAAGAACAAACAA 3008
QY 3156 TCACCGTCTCTGCTGTTATCCAGAAATGGGAAGCAGAGTGTCAACAGCAGTTCGCT 3215
Db 3009 CCAACGTTTCGCTCTGCTGTTCCGNAATGGGAAGCAGAGTGTCAAGNAAGTTCGCT 3068
QY 3216 CTGTCGGGGCGGTGCTATATCTCCGTGTCAAGGTACAAGAGGGATATGGAAGGG 3275
Db 3069 CTGTCGGGGCGGTGCTATATCTCCGTGTCAAGGTACAAGAGGGATATGGAAGGG 3128
QY 3276 TTGTGTAACCATCATGAAATCGAGAACATACAGACGAATCAAAATTTAAACCTGTGA 3335
Db 3129 TTGGTAAACATTCATGAGATCGAAGAACATACAGACGAATCAAAATTTAGCAACTGGT 3188
QY 3336 AGAAGAGGAGTGTATCCAAACGAGTACAGGAACGTTGATGATTAATCTGCAACCAAGG 3395
Db 3189 AGAAGAGGAAATCTATCCAAATAACACGCTAACGTTGATTAATCTGTAATCAAGA 3248
QY 3396 TACAGCAGTATGTAATTTCCCGTAAATGCTGGATATGAGGATGATTAAGATTGATPAC 3455
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Db 3249 AGAATACGGAGTCCGT-----ACACTTCGTAAATCGAGGATATATACGAAGCTCCTTC 3302
QY 3456 AGCATCTGTTAAATTAACAAACCGACTTATGAAGAAAGAAACGTATACAGATGTACGAAGAGA 3515
Db 3303 CGTACCAGCTGATTTATCGCTCAGTCTATATGAAGAAATCGTATACAGATGCGAAGAGA 3362
QY 3516 TAATCATTTGTAATATACAGAGGGTATGTGAATTAATCCACCTACCACTGCTGTTATAT 3575
Db 3363 GAATCCTTGTGAATTTAAACAGAGGGTATAGGGATTTACCGCCACTACCACTGCTGTTATGT 3422
QY 3576 GACAAAAAGAAATTAGAAATTAATCTCCAGAAACCGATTAAGGTATGATTTGAGATTGAGAAAC 3635
Db 3423 GACAAAAAGAAATTAGAAATTAATCTCCAGAAACCGATTAAGGTATGATTTGAGATTGAGAAAC 3482
QY 3636 GGAAGGGAAGTTTATTTGTAGACAGCGTGGAAATTAATCTCTTATGAGGAATAG 3687
Db 3483 GGAAGGGAACATTTTATCTGTGACAGCGTGGAAATTAATCTCTTATGAGGAATAG 3534

RESULT 12
US-09-997-914-25
; Sequence 25, Application US/09997914
; Publication No. US20030119158A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum d-Endotoxins
; FILE REFERENCE: 11792.0215.DVUS01 MECO:215--1
; CURRENT APPLICATION NUMBER: US/09/997,914
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/261,040
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)...(3531)
US-09-997-914-25

Query Match 38.0%; Score 1402; DB 10; Length 3534;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;

QY 285 TCAGTGGGAATTTTCTCTAGAACATGTCGAACAACTTATAAATCAACAAATAACAGAAAA 344
Db 213 TCAATGGGACGCAATTTCTGTACAAATTGAACAGTTAAATTAACCAAGAAATAGAAGATT 272
QY 345 TGCTAGGAATACCGCACTTGTCTGATTACAAGGTTTAGGAGATTCCTTTAGAGCCTATCA 404
Db 273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAGCACTAAGCAATCTTTATCAAAATTACGC 332
QY 405 ACAGTCACTTGAGATTGGCTAGAAAACCGTGATGATGCAAGAACGAGAGAGTGTCTTTA 464
Db 333 AGAATCTTTTAGAGAGTGGGAAGCAGATCCTACTAATCCAGCATTAAGAGAGAGATGCG 392
QY 465 TACCAATATATAGCCTTAGAACTTCGATTTCTTAATGCGATGCCCTTTTGCATTTAG 524
Db 393 TATTCATTCATGACATGACAGTGCCTTACACCGCTATTTCTCTTTTTCAGTTCA 452
QY 525 AAACCAAGAGTTTCCATTTAATGTTATATGCTCAAGCTGCAAAATTTACACCTATT 584
Db 453 AAATTTATCAAGTTCTCTTTTATCAGTATATGTTCAAGCTGCAAAATTTACATTTACGT 512
QY 585 ATTGAGAGATGCTCTCTTTTGGTGTAGTGAATTTGGGCTTACATGCGAGAAATTCACG 644
Db 513 TTTGAGAGATGTTTCAGTGTTTGGCAAAAGGTGGGATTTGATGCGCGACTATCAATAG 572
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QY 3216 CTGTCGGGGCGTGGCTATATCTCCGTGTCTACAGCGTCAAAAGAGGATATGGAGGG 3275
Db |||||
QY 3069 CTGTCGGGTCGGGTATATCTTCGTGTCAAGCGTCAAGGAGGATATGGAGAGG 3128
Db |||||
QY 3276 TTGTGTAACGATCCATGAATCGAGAACAAATACAGACGAACTTAAATTTAAAACTGTGA 3335
Db |||||
QY 3129 TTGGTNAACATTCATGAGTCTGAGAACAAATACAGACGAACTTGAAGTTTGAACACTGCGT 3188
Db |||||
QY 3336 AGAAGAGGAAGTGTATCCAAACCGATACAGGAACGTTGTAATGATTATATCTGCACACCCAAAGG 3395
Db |||||
QY 3189 AGAAGAGGAATCTATCCAAATACACAGGTAAAGTGTATGTTATATCTGTAAATCAAGA 3248
Db |||||
QY 3396 TACAGCAGTATGTAATCCCGTAAGTCTGGATATGAGGATGATATGAAGTTGATATCTAC 3455
Db |||||
QY 3249 AGAATACGAGAGTGGCT-----ACACTTCTCGTAATCGAGGATATAACGAAAGCTCCTTC 3302
Db |||||
QY 3456 AGCATCTGTTAATTAACAAACCGACTTATGAAGAGAAACGTTATACAGATGTACCAAGAGA 3515
Db |||||
QY 3303 CGTACCAGCTGATTATGCGTCAGTCTATGAAGAAATCTGTATACAGATGGACCAAGAGA 3362
Db |||||
QY 3516 TAATCATTTGTGAATATGACAGAGGATGTGAATATATCCACATACAGCTGGTTATAT 3575
Db |||||
QY 3363 GAATCCCTTGTGAATTTAAACAGAGGATATAGGATTTACACGCCACTACCCAGTTGGTTATGT 3422
Db |||||
QY 3576 GACAAAGAAATTAGAATACTTCCAGAAACCGATAAGGTATGGAATTCAGATTCGAGAAAC 3635
Db |||||
QY 3423 GACAAAGAAATTAGAATACTTCCAGAAACCGATAAGGTATGGAATTCGAGATTCGAGAAAC 3482
Db |||||
QY 3636 GGAAGGGAAGTTTATTTGATAGACAGCGTGGAAATTAATCTCTTATGGAGGAATAG 3687
Db |||||
QY 3483 GGAAGGAACATTTATTCGTGGACAGCGTGGAAATTAATCTCTTATGGAGGAATAG 3534
Db |||||

RESULT 14

US-10-672-163-25
; Sequence 25, Application US/10672163
; Publication No. US20040093637A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum
; FILE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 11792.0215.DVUS02 MECO:215--2
; CURRENT APPLICATION NUMBER: US/10/672,163
; PRIOR FILING DATE: 2003-09-26
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/997,914
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 08/261,040
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-10-672-163-25

Query Match 38.0%; Score 1402; DB 16; Length 3534;
Best Local Similarity 65.7%; Pred. No. 0;
Matches 2243; Conservative 0; Mismatches 1070; Indels 99; Gaps 10;
QY 285 TCAGTCGGGAATTTCTCTAGACATGTCGAACAACTTATAAATCAACAAATTAACAGAAA 344
Db |||||
QY 213 TCAATGGGACGCAATTTCTTGTCAAAATTTGAACAGTTAATTAACCAAGAAATAGAGAAT 272
Db |||||

QY 345 TGCTAGGAATACGGCACTTCTCGATTACAAAGCTTTAGGAGATTCCTTTAGAGCCTATCA 404
Db |||||
QY 273 CGCTAGGAACCAAGCCATTTCTAGATTAGAAAGACTAAAGCAATCTTTATCAAAATTTACGC 332
Db |||||
QY 405 ACAGTCACTTTGAAGATTTGGCTAGAAAACCGTGTATGATGCAAGAACGAGAAAGTGTCTTTTA 464
Db |||||
QY 333 AGAATCTTTTAGAGAGTGGGAAGCAGATCTCTACTAATCCAGCATTAAGAGAAGAGATGCG 392
Db |||||
QY 465 TACCCATATATAGCCTTAGAAGTGTATTTCTTAATGCGATGCCCTTTTTCGCAATTAG 524
Db |||||
QY 393 TATTCAAATTCAAATGACATGAACAGTCCCTTACAAACCGTATTTCTCTTTTTCAGTTCA 452
Db |||||
QY 525 AAACCAAGAGTTTCCATTAATATGATATGCTCAAGCTGCAAAATTTTACACCTATATTT 584
Db |||||
QY 453 AAATATCAAGTTCTCTTTTATCAGTATATGTTCAAGCTGCAAAATTTTACATTTATCAGT 512
Db |||||
QY 585 ATTGAGAGATGCCCTCTCTTTTGGTATGAAATTTGGGCTTATCATCGCAGGAATTTCAACG 644
Db |||||
QY 513 TTTGAGAGATGTTTCAAGTGTGTTGGACAAAGTGGGATTTGATGCCGCGACTATCAATAG 572
Db |||||
QY 645 TTATATGAGCGCAAGTGGAAACAAACGAGAGATTTATCCGACTATTTGCTAGATGGTA 704
Db |||||
QY 573 TCGTTATATGATTTAACTAGGCTTATTGGCAACTATACAGATCATGCTGTACGCTGGTA 632
Db |||||
QY 705 TAATACAGGCTTAATATGCTTGAAGGGAACAATGCCCAAGTTGGGTCGCTTATAATCA 764
Db |||||
QY 633 CAATACGGGATTAGAGCGTGTATGGGACCGGATTTCTAGAGATTTGATAAGATATAATCA 692
Db |||||
QY 765 ATTCCGTCAGAGATCTAAAGTGTAGGCGTATAGATCTAGTGGCACTATTTCCCAAGCTATGA 824
Db |||||
QY 693 ATTGAGAGAAATTAACACTAACTGTATAGATATCGTTTCTCTATTTCCGAACATGA 752
Db |||||
QY 825 CACTCGCACTTATCCAATAAATACGAGTGTCTCAGTTAAACAGGGAAGTTTATACAGACGC 884
Db |||||
QY 753 TAGTAGACGTATCCAATTCGAACAGTTTCCCAATTAACAGAGAAATTTATCAAAACC 812
Db |||||
QY 885 A--ATTGGAGCAACAGGGTAAATATGCAAGATATGAATTTGTTATAATAATGCACT 942
Db |||||
QY 813 AGTATTAGAAATTTTGAAGTAGTTTTCGAGGCTCGGCTCAGGCGATAGAAAGATAT 872
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QY 943 TCGTTTTCGCTATAGAGACTGCGGTTATCCGAAGCCGCACTACTTTGATTTTCTAGAA 1002
Db |||||
QY 873 TAGGAGTCCACATTTGATGGATATATTAACAGTATACCATCTATACGAGTGTCTATAG 932
Db |||||
QY 1003 CAATTTACAAATTTTAGCACTTCTATCAGATGGAGTGTCTACTAGGCATATAGACTTACTGG 1062
Db |||||
QY 933 GGGTTATTATTATTGGTTCAGGGCATCA-----AATAATGGCTTCTCTGTAGGGTT 983
Db |||||
QY 1063 CGGGGCGACACAATTCATCTCGGCCAATAGGAGCGGATTAATACTCTCAACGCACTGGG 1122
Db |||||
QY 984 TTCGGGCGCAGAAATTCATTTTCGCTATATGGAACATATGGGA-----ATGCA 1032
Db |||||
QY 1123 TCTACCAATATCTTATTAATCTCTGTGAAGATTTATCATTTCTCTCGAGAGCTATATGG 1182
Db |||||
QY 1033 GCTCCACAACAAACGTTATTTGCTCAACTAGGTCCAGGCGGTATAGAACATATCGTCC 1092
Db |||||
QY 1183 ACTGAATCATATGCAAGGAGTCTTCTATGGGAATTTACCTTGAACCTTATCATGTGTCT 1242
Db |||||
QY 1093 ACTTTATATAGAAGACCTTTTAATATAGGGATAAATAATCAACCACTATCTGTCTTGGAC 1152
Db |||||
QY 1243 CCTACTGTATGATTTAAATTTTAGGAACCTCTCAGAAATACTTTTGAAGAGGTTACTGTGAAC 1302
Db |||||
QY 1153 GGGAC---AGAAATTTGCTTATGGAACTCTCTCAAAATTTGCCATCCGCTGTATACAGAA 1208
Db |||||
QY 1303 TATAGTCAACCTATGATGACCTGGGCTTCAATTTAAAGATTCAGAAACCTG--AATFACC 1361
Db |||||
QY 1209 AAGCGGAACGGTAGATTCGCTGGATGAATTAACGCCACAGAAATAACACGTCGCCACCTAG 1268
Db |||||
QY 1362 ACCAGAAACCAACAGAACGCAAAATTAATGAATCATATAGTCATAGGTTATCTTCACATAGG 1421
Db |||||
QY 1269 GCAAGGATTTAGTCACTGATTAAGCCATGTTTCAATGTTTCTGT-----TCAGGCTTTAG 1322
Db |||||
QY 1422 GCTCATTTTCAATCTAGGTCATGTACCAAGTATATTTCTTGGACGCACTGTATGCAGA 1481
Db |||||

Db 1323 TAATAGTAGTGAAGTATTAATAGAGCTCCAATGTTTTCTTGGACGCAACCGTAGTGAAC 1382
Qy 1482 TGGTCAAAATACCATTTAGTTCAGATAGCATACACAAATACCATTTGGTAAATCATTCNA 1541
Db 1383 CCTACAAATACAAATTTGATCCGGAGAGGATTAATCAATACCATTTGGTAAAGGACATAC 1442
Qy 1542 CTTAAATCCAGGTACCTCTGTAGTCAGTGGCCAGGATTTACAGAGGGGATATATCCG 1601
Db 1443 ACTTCAGTCAGGTACTACTGTTGTAAGAGGCGCGGTTTACGGGAGGATATTTCTCG 1502
Qy 1602 AACTAACGTTAATGTAGTGTACTAAGTATGGGTCTTAAATTTAATAATACATCATAC 1661
Db 1503 ACGAAACAGTGGAGGACCAATTTGCTTATATCTATTTGTTAATAATAAATGGGCAATTA 1562
Qy 1662 GGGGTATCGGTGAGAGTTCGTTATGCTGCTTCTCAAAACAATGGTCTCGAGGGTAACTGT 1721
Db 1563 AAGGTATCGTGCAGATACGCTATGCTCTACTACAAATCTAAGAAATTTAGTAACGGT 1622
Qy 1722 CGAGGGAGTACTACTTTTGTATCAAGGATTCCTTAGTACTATAGAGTGCAAAATGAGTCTTT 1781
Db 1623 TCGAGGTGAACGGATTTTGTGCTGCTCAATTTAAACAAACAATGGATACCGGTGACCCATT 1682
Qy 1782 GACATCTCAATCATTTAGATTTGCGAATTTCTCTGTAGGTATTTAGTGCAATCTGGCAGTCA 1841
Db 1683 AACATTTCCAATCTTTTAGTTACGCAACTATTAATACAGCTTTTATCAATCCCAATGAGCCA 1742
Qy 1842 AACTGCT---GGAATAAGTATAAGTAATAATCGAGGTAGCAAAAGTTCATTTGATAA 1898
Db 1743 GAGTAGTTTCA CAGTAGGTGCTGTA CTTTGTAGTTCAAGGAATGAAGTTTATATAGACAG 1802
Qy 1899 AATTGAAATTCATTTCCAATTTACTGCAACCTTTCCGAAGCAGAAATACGATTTAGAAAGGCGCA 1958
Db 1803 ATTTGAAATTTGATTTCCAGTTACTGCAACATTTGAGCAGAGATATGATTTAGAAAGAGCACA 1862
Qy 1959 AGAGCGGTGAATGCTCTGTTTATTAATACGAATCOAAGAAAGATTTGAAACAGAGTGTGAC 2018
Db 1863 AAAGCGGTGAATGCGCTGTTTACTTCTATAAACCAATAGGGAATAAAACAGATGTGAC 1922
Qy 2019 AGATTTATCATATTTGATCAAGTATCCAAATTTAGTGGCGGTTTATCGGATGAATTCGCTT 2078
Db 1923 GATTTATCATATTTGATCAAGTATCCAAATTTAGTGGATTTGTTTATCAGATGAATTTGTCT 1982
Qy 2079 AGATGAAAGAGAGAAATTAATTTGAGAAAGTGAATATCGAAACGACTCAGTGTAGAAAG 2138
Db 1983 CGATGAAAGCGAGAAATTTGTCGAGAAAGTCAACATCGGAAGCGACTCAGTGTAGCGG 2042
Qy 2139 AAATTTACTCCAGATCCAACTTCCATCCATTAATAGCAACAGCACTTCATATCTAC 2198
Db 2043 GAAATTTACTCAAGATCCAACTTCAAGGCAATCAATAGGCAACTAGAC----- 2091
Qy 2199 TAATGAGCAATCGAATTTACATCTATCCATGAACAATCTGNAACATGGATGTTGGGAAG 2258
Db 2092 -----CGTGGTTGGAGAGGAAG 2108
Qy 2259 TGAGAACATTTAAATCCAGGAAGAAATGACGTATTTAAAGAGAAATTAAGTACCACTACC 2318
Db 2109 TACGGATATACCATCCAAAGAGGAGATGACGTATTTCAAGAAATTTATGTCACTACC 2168
Qy 2319 GGGGACTTTTATAGTGTATCCGACGTATTTATATCAAAATAAGAGAGTCCGAAT 2378
Db 2169 AGGTACCTTTGATGAGTGTATCCAAACATATTTGATCAAAAAATCGATGAATCAAAAT 2228
Qy 2379 AAAAGCTTACTCCCTACCAATTAAGGGTATATTTGAAGTATGATCAAGATTTAGAT 2438
Db 2229 AAAAGCTTTTACCGTTATCAATTTAAGAGGGTATATCGAAGATAGTCAAGACTTTAGAAAT 2288
Qy 2439 ATATTGATTCGTTAATGCGAAACATGAACATTTGGATTTTCAGAGTACCGAGTCCGT 2498
Db 2289 CTAATTTAATTCGTTACATGCAAAACATGAACAGTAAATGTGCCAGGTACGGGTTCTTT 2348
Qy 2499 ATGGCCGCTTTTCAGTTGAAGCCCAATCGGAAGGTGCGGAGAACCGAATTCGATGCGACC 2558

Db 2349 ATGGCCGCTTTTCAGGCCAAAGTCCAAATCGAAAGTGTGGAGAGCCGAATCGATGCGCGC 2408
Qy 2559 ACATTTTCAATGGAAATCTGATCTAGATTTGTTCTGCGAGAGATGAGAAAAATGTCGCGCA 2618
Db 2409 ACACCTTGAATGGAAATCTGATCTAGATTTGTTCTGTTAGGGATGAGAAAAAGTGTGCCCA 2468
Qy 2619 TCATTTCCCATCATTTCTCTTTGGATTTGATTTGCGATGCGACAGACTTGTGCATGAGAACT 2678
Db 2469 TCATTTCCCATCATTTCTCTTTAGACATTTGATGCTAGAGTGTACAGACTTTAAATGAGACCT 2528
Qy 2679 AGGCGTGGGTGATTTCAAGATTTAAGACGAGAGGTCATGCAAGCTAGGGAATCT 2738
Db 2529 AGGTGTATGGGTGATCTTTAAGATTTAAGACGCAAGATGGGCAACGCAAGACTAGGGAATCT 2588
Qy 2739 GGAATTTATTCGAAGAGAAACCAATTTATAGGAGAGCACTGTCTGCTGTCGAGAGAGCAGA 2798
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Qy 2919 TACAAACATTCGCATGATTCATGCGGAGATTAATCTGTTCTCATCGAATTCGAGAGCTTTA 2978
Db 2769 TACGAATATTCGCATGATTCATGCGGAGATTAATCTGTTCTCATGCAATTCGAGAGACTTTA 2828
Qy 2979 TCTGTCAAGATTTATCTGTTATCCCGGTGTAAATGCGGAAATTTTGAAGAAATTAAGAAG 3038
Db 2829 TCTGCTGAGCTGTCTGTGATTCGGGTGTCAATGCGGCTATTTTGAAGAAATTAAGAAG 2888
Qy 3039 TCGCAATATCACTGCAATCTCCCTATACGATGCGAGAAATGTCGTTAAATAATGTTGATTT 3098
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Qy 3099 TAATAAGTATGATTCGATTCGAAATGTAAGAGGCAATGATGTAGATGTAGAGAAACAAACAA 3155
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Qy 3156 TCACCGTTCTCTCTCTGTTATCCAGAAATGGAAGCAGAGTGTCAAGCAGATTCGCGT 3215
Db 3009 CCAAGTTGCGTCTCTGTTGTTCCGGAATGGAGCAGAGTGTCAAGAGATTCGTT 3068
Qy 3216 CTGTCGGGGCGTGGCTATATCTCTGCTGTCAAGCGTCAAAAGAGGATATGAGAGAGG 3275
Db 3069 CTGTCGGGGCGTGGCTATATCTCTGCTGTCAAGCGTCAAGAGGAGGATATGAGAGAGG 3128
Qy 3276 TTGTTAAGCATCCATGAAATCGAGAAACAAATACAGACGAACTTAATAATTTAANAATGTGA 3335
Db 3129 TTGCGTAACCAATCATGAGATCGAGAAACAAATACAGACGAACTGAAGTTTAGCACTCGGT 3188
Qy 3336 AGAAGAGAAAGTGTATCCAAACGATACAGGAACGTTGATGATTTATATCTGCACACCAAGG 3395
Db 3189 AGAAGAGAAATCTATCCAAATACACGTTAAACGTTGATGATTTATCTGTAAATCAAGA 3248
Qy 3396 TACAGAGTATGTAATTTCCCGTAAATGCTGGATATGAGGATGATATGAAGTTGATATCTAC 3455
Db 3249 AGAATA CGGAGGTGCGT-----ACACTTCTCGTAAATCGAGGATATAACGAAGCTCCTTC 3302
Qy 3456 AGCATCTGTTAATTTACAAACCGACTTATGAGAGAGAAACGATATACAGATGTACGAGAGA 3515
Db 3303 CGTACCAGCTGATTTAGCGTCAGTCTATGAAGAGAAATCGTATACAGATGGAACGAAGAGA 3362
Qy 3516 TAATCATTTGTAATGACAGAGGATGTAATTTATCCACCACTTACCAAGCTGCTGTTATAT 3575
Db 3363 GAATCTCTGTAATTTAAGAGAGGATGAGGATTTACCGCACTACCAAGTTGTTGTTATGT 3422
Qy 3576 GACAAAAAGAAATTAAGATACTTTCCAGAAACCGAATAAGGTATGGATTTGAGATTTGGAGAAAC 3635
Db 3423 GACAAAAAGAAATTAAGATACTTTCCAGAAACCGAATAAGGTATGGATTTGAGATTTGGAGAAAC 3482

Db 1683 AACATTCCAATCTTTTAGTTAGCGCAACTATTAAATACAGCTTTTACATTCCTCCAAATGAGCCA 1742
Qy 1842 AACTGCT---GGAATAAGTATAAGTAATAATGTCAGGTAGACAAACGTTTCTACTTTGATAA 1898
Db 1743 GAGTAGTTTCACAGTAGTGCTGATACCTTTTAGTTTCAGGGAATGAAGTTTATATAGACAG 1802
Qy 1899 AATTGAATTCATTCCTCAATTTACTGCAACCTTCGGAAGCAGAAATACGATTTAGAAAGGCGCA 1958
Db 1803 ATTTGAATTTGATTCAGTTACTGCAACATTTTGAAGCAGAAATATGATTTAGAAAGAGCACA 1862
Qy 1959 AGAGCGGTGAATGCTCTGTTTACTTAATACGAATCCAAGAGATGGAAGAACAGATGTGAC 2018
Db 1863 AAAGCGGTGAATGCGCTGTTTACTTCTATAAACCAAAATAGGGAATAAAACAGATGTGAC 1922
Qy 2019 AGATTATCATATTGATCAAGTATCCAAATTTAGTGGCGTGTATTCGGATGAATCTGCTT 2078
Db 1923 GGAATTATCATATTGATCAAGTATCCAAATTTAGTGGATTTGTTTATCAGATGAATTTGTCT 1982
Qy 2079 AGATGAAGAGAGAAATTTACTTTGAGAAAGTGAATAATCGGAACGACTCAGTGATGAAG 2138
Db 1983 GGATGAAGAGAGAAATTTGTCGGAAGAGTCAAAATCGGAAGCGACTCAGTGATGAGCG 2042
Qy 2139 AAATCTACTCCAAGTCCAAATCTTCAATCATCATCAATGAAGCAACAGACTTCATATCTAC 2198
Db 2043 GAATTTACTTCAAGATCCAAATCTTCAAGGCGATCAATAGGCACTAGAC----- 2091
Qy 2199 TAATGAGCAATCGAATTTTCAATCTATCCATGAACAAATCTGAACATGATGATGGGGAAG 2258
Db 2092 -----CGTGGTTGGAGGGAAG 2108
Qy 2259 TGAGAACATTAATCCAGGAGGAAATGACGTATTTAAAGAGAAATACGTCACTAC 2318
Db 2109 TACGGATATTACCATCCAAAGAGGAGATGACGTATTTCAAGAGAAATATATGTCACTACC 2168
Qy 2319 GGGGACTTTTATGAGTGTATCCGACGTATTTATATCAAAATAGGAGTCCGAAAT 2378
Db 2169 AGGTACCTTTGATGAGTGTATCCAAACATATTTTGTATCAAAATTCGATGAATCAAAAT 2228
Qy 2379 AAAAGCTTTATCTCGCTACCAATTAAGAGGGTATATTCAGATAGTCAAGATTTAGAGAT 2438
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Qy 2439 ATATTTGATTCGTTAATGCGAAACATGAACATTTGGATGTTCCAGGTACCGAGTCCGT 2498
Db 2289 CTATTTAATTCGTACAAATGCAAAACATGAACAGTAAATGTGCCAGGTACGGGTTCTCT 2348
Qy 2499 ATGGCGGCTTTTCAAGTGAAGCCCAATCGGAAGGTGCGGAGAACCGAATCGATGCGCAC 2558
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Qy 2559 ACATTTTGAATGGAATCTGATCTAGATTTGTTTCTGTCAGAGATGAGAGAAATGTGCGCA 2618
Db 2409 ACACCTTGAATGGAATCTGATCTAGATTTGTTTCTGTTAGGATGAGAGAAATGTGCGCCA 2468
Qy 2619 TCATTTCCATCATTTCTCTTTTGGATTTATGATTTGGATGSCAGACTTTGCAATGAGAATCT 2678
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Db 3069 CTGTCCGGGCGTGGCTATATCTCTCGTGTCAACAGCGTACAAAGAGGATATGGAGGG 3128
Qy 3276 TTGTGTAAACGATCCATGAAATCGAGAAACAAATACAGACGAACTAAAATTTAAAAA 3335
Db 3129 TTGCGTAACCATTCATGAGATCGAGAACAAATACAGACGAACTGAAGTTTAGCACTGCT 3188
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Qy 3576 GACAAAGAAATTAAGAAATCTTCCAGAAACCGATAGGTATGGAATGGAAGAGAGAG 3635
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Qy 3636 GGAAGGAGAAATTTATTTAGACAGCTGGAATTTACTCTTATGAGGAGAAATAG 3687
Db 3483 GGAAGGAGAAATTTATTTAGACAGCTGGAATTTACTCTTATGAGGAGAAATAG 3534

Search completed: November 21, 2004, 16:50:28
Job time : 1775 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 08:54:06 ; Search time 10040 Seconds
(without alignments)
13381.802 Million cell updates/sec

Title: US-10-614-524-1
Perfect score: 3687
Sequence: 1 ttgacttcaaatagaaaaa.....tactcttatggaggaatag 3687

Scoring table: IDENTITY_NUC
Gapop 10.0., Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	1.7	880	8	AZ669474
2	59	1.6	908	8	AZ548467
3	57.4	1.6	843	8	AZ551618
4	55.8	1.5	748	9	BX137558
5	55.2	1.5	931	8	BH160272
6	52.8	1.4	1101	9	CNS0039G
7	52.4	1.4	877	8	AZ531291
8	52	1.4	849	8	AZ546009
9	51.8	1.4	886	5	BX422107
10	51.8	1.4	1101	9	CNS008VL
11	51.2	1.4	900	8	AZ549980
12	51	1.4	1101	9	CNS008MH
13	51	1.4	1337	9	AG280055
14	50.6	1.4	912	8	AZ551092
15	50.2	1.4	467	4	BM163521
16	49.8	1.4	1253	9	AG289789
17	48.8	1.3	1064	4	BM416119
18	48.6	1.3	890	8	AZ530768
19	48.4	1.3	543	4	B1397189
20	48.4	1.3	905	8	AZ550256
21	48.4	1.3	1101	9	CNS0106X
22	47.6	1.3	828	8	AZ669217
23	47.6	1.3	906	8	AZ529180
24	47.6	1.3	939	8	AZ540454

25	47.6	1.3	1101	9	CNS0100X
26	47.4	1.3	654	4	BM164708
27	47.4	1.3	997	9	CNS005TE
28	47	1.3	811	4	BJ403374
29	47	1.3	976	8	BH149983
30	46.8	1.3	531	4	BJ363051
31	46.8	1.3	568	4	BJ363776
32	46.8	1.3	582	4	BJ366397
33	46.8	1.3	782	9	AG444032
34	46.8	1.3	1101	9	CNS0026Z
35	46.8	1.3	1307	9	AG347197
36	46.6	1.3	537	5	BU498625
37	46.6	1.3	548	4	BI670654
38	46.6	1.3	556	4	BI814240
39	46.6	1.3	585	5	BU496406
40	46.6	1.3	921	8	BH149893
41	46.4	1.3	680	4	BJ384484
42	46.4	1.3	683	4	BJ386441
43	46.4	1.3	826	4	BJ383101
44	46.4	1.3	875	8	AZ671853
45	46.2	1.3	609	4	BJ444006

ALIGNMENTS

RESULT 1
AZ669474
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ669474
ENTY188TR Entamoeba histolytica Sheared DNA linear GSS 14-DEC-2000
genomic, genomic survey sequence.
AZ669474
GSS.
Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 880)
Loftus B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 22
High quality sequence stop: 853.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHO51; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome

Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999).

ORIGIN

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Query Match      1.7%; Score 61; DB 8; Length 880;
Best Local Similarity 46.4%; Pred. No. 0.00037;
Matches 199; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 3252 GTACAAGAGGGATATGGACAGGGTGTGTAAACGATCCCAATCGAGACAAATACAGA 3311
Db 12 GTAAGGAGAGAGATGAAGATGATGATGAAGAGAGAGATGAAGATGATGATGAAGA 71
QY 3312 CGAACTAAATATTTAAATACTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3371
Db 72 AGATGATGATGAAGAGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 131
QY 3372 TAATGATTATACGCACCAAGGTACAGCAGTATGTAATTCCTGTAATGCTGGATGA 3431
Db 132 AGAAGATGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191
QY 3432 GGATGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3491
Db 192 AGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251
QY 3492 AACGTATACAGATGTACGAGAGAGATTAATCACTGTAATATGACAGAGGGTATGTGAATTA 3551
Db 252 TGATGATGAAGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
QY 3552 TCACCACTACAGCTGGTGTATATGACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 3611
Db 312 TGAAGATGATGAAGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
QY 3612 GGATGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3671
Db 372 TGATGAAGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
QY 3672 CCTTATGGA 3680
Db 432 CTATGATGA 440
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RESULT 2
LOCUS AZ548467
DEFINITION ENTX30TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.

ACCESSION AZ548467
VERSION AZ548467.1
KEYWORDS GSS.
SOURCE GI:11172102

ORGANISM Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 908)
AUTHORS Loftus, B., Van Aken, S. and Fraser, C.
TITLE Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library

JOURNAL Unpublished (2000)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208
Fax: 301 838 3543
Email: bjl@tifg.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library

Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 828.

Location/Qualifiers
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/organism="Entamoeba histolytica"

FEATURES
Source

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/clone_lib="Entamoeba histolytica Sheared DNA"  
/note="Vector: pHS1; Site 1: Bat I; Constructed at The  
Institute for Genomic Research (TIGR), Rockville, MD.  
Genomic DNA isolated from broth cultures of E. histolytica  
using a method described by Clark and Diamond (Clark, a  
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a  
method for isolate identification. Exp. Parasitol.  
77:450.). The DNA was mechanically sheared to give a  
tight size distribution (~2 kb). The v + i method used for  
the library construction is described in detail in Smith,  
H.O. and Venter, J.C. (Making small insert libraries for  
whole genome shotgun sequencing projects. In Genome  
Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barell, Oxford University Press, 1999)."
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ORIGIN

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Best Local Similarity 44.2%; Pred. No. 0.0012;  
Matches 337; Conservative 0; Mismatches 420; Indels 6; Gaps 2;  

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Db 66 AGAAGATGATGATGAAGAGAGATGATGATGATGAAGAGAGATGATGAAGAGATGATGAAGA 125
QY 2853 TACAGAGGCAAAAGAGCTGTGGATCTTTATTTGTAGATCTCTCAATATAATAGATTACA 2912
Db 126 AGAAGAGAGATGATGAAGATGAAGATGATGAAGACCATGAAGACGACGAATATGAATTAGA 185
QY 2913 ACGGATACAAACATTTGGCATGATTCATCGGCAGATAACTTGTTCATCGAATTCGAGA 2972
Db 186 AGATGATG---ATGATGAAGAGAGAGAGATGATGATGAAGATGATGAAGACGATGAAGA 242
QY 2973 GGCCTATCTGTGAGAAATATCTGTTATCCCGGTGTAAATGCGGAAATTTTGAAGAAAT 3032
Db 243 CGACGAATATGAATTAGAAGATGATGATGATGAAGAGAGAGATGATGATGAAGAGAGA 302
QY 3033 AGAAGTCGCATATATCACTGCAATCTCCCTATACGATGCGAGAGAAATGTCGTTHAAATGG 3092
Db 303 AGAAGATGATGATGAAGATGATGATGAAGAGAGAGATGATGAAGAGAGATGATGAAGAGATGA 362
QY 3093 TCATTTTATAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3152
Db 363 TGAAGATGATGATGAAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 422
QY 3153 CCATCACCGTCTCTGTCCTTTATCCGAATGGGAAGCAGAGAGTGTCTCAAGCAGTTCG 3212
Db 423 CGAATATGAATTAGAAGATGATGATGAAGAGAGAGATGATGATGAAGAGAGAGAGA 482
QY 3213 CGTCTGTCGGGGCGGTGGCTATATCTCGTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3272
Db 483 TGATGATGAAGATGATGATGAAGAGAGAGATGATGAAGAGAGAGATGATGAAGAGAGAGATGA 542
QY 3273 GGGTTGTGAACGATCCATGAAATCGAAGACA---ATACAGAGCAACTAAATTTAAAAA 3329
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QY 3330 CTGTGAAGAGAGAGAGAGTGTATCCACCGGATACAGGAACGTCGTATATGATTAATCTGACA 3389
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/note="vector pIndigoBAC-536"

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p>	<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p>

**JOURNAL
COMMENT**

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ORIGIN
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Best Local Similarity 15.7%; Pred. No. 0.05;
Matches 99; Conservative 264; Mismatches 269; Indels 0; Gaps 0;
/next-end : 1113

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FEATURES

ORIGIN

Query Match
Best Local
Matches

Qy Db

Qy nb

Qy

 $\partial \gamma$

Qy

Qy Db

Db Oy

db

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p>	<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p>

FEATURES

ORIGIN

Query Match
Best Look
Matches

Qy Db

Qy Db

Qy Dp

 $\frac{dy}{dx}$

Qy

3

Qy

Db

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RESULT 8
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LOCUS ENTFW53TF Entamoeba histolytica Sheared DNA linear GSS 14-NOV-2000
DEFINITION genomic, genomic survey sequence.
ACCESSION A2546009
VERSION A2546009.1 GI:11167130
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
REFERENCE Eukaryota; Entamoebidae; Entamoeba.
AUTHORS 1 (bases 1 to 849)
Loftus, B., Van Aken, S. and Fraser, C.
TITLE Determination of clone end sequences from Entamoeba histolytica
JOURNAL HMI:IMSS sheared DNA library
COMMENT Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 26
High quality sequence stop: 796.
Location/Qualifiers
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/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Best Local Similarity 43.3%; Pred. No. 0.075;
Matches 296; Conservative 0; Mismatches 385; Indels 3; Gaps 1;
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DB 734 AGATGAAATGTAGAAATGCAATGATACCGTTAGAGCAATGAATTAGAAGAAGA 675
QY 2871 TGTGGATGCTTTATTTG----TAGATCTCAATATATAGATTACAAGCGGATACAAACAT 2927
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QY 2928 TGGCATGATTCATGCGCGCAGATAAACTTCTTCATCGATTTCAGAGGCTTATCTGTCTAGA 615
DB 614 AGATGAAGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2987
QY 2988 ATTATCTGTATCCCGGGTGAATTCGCGGAAATTTTGAAGAATTTAGAAAGGTTCGCATTAT 3047
DB 554 ATTAGAAGATGAAGAGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 495
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QY 3168 CTTTGTATCCAGATGGGAAGCAAGTGTCAACAGCAGTTTCGGGTCTCTGTCGCGGGCG 3227
Db 374 AGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGA 315
QY 3228 TGGCTATATCCTCGTGTACACGCTACAAAGAGGATATGGAGAGGTTGTGTAAACGAT 3287
Db 314 TGATGATGATGATGAAGATGAAGAAGATGATGATGAATTTGAATTTAGAAGATGA 255
QY 3288 CCATGAATCGAACAATAACAGACGAACCTAAATTTAAAACTGTGAAGAAGAGGAAGT 3347
Db 254 AGAAGATGAAGATGATGAAGACGAAGACGAAGATGATGATGAATTTGAATTTAGA 195
QY 3348 GTATCCAAACGATACAGGACGTTGTAATGATTATCTGCACACCAAGGTACAGCAGTATG 3407
Db 194 AGATGAAGATGAAGATGAAGAAGATGAAGAAGATGATGAAGAAGAAAGAAGA 135
QY 3408 TAATTCCTTAATGCTGGATATGAGGATGCATATGAAGTTGATCTACAGCATCTGTTAA 3467
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QY 3468 TTACAACCGACTTATGAAGAAGA 3491
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RESULT 9
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LOCUS BX422107 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA
DEFINITION clone CS0DH007YD10 3-PRIME, mRNA sequence.
ACCESSION BX422107
VERSION BX422107.2 GI:46930727
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30651307.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
division of Invitrogen.
This sequence belongs to sequence cluster 3628.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DH007YD10SNP1&c=3628.r.
FEATURES
Location/Qualifiers
1..886
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DH007YD10"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/cell_line="JURKAT CELL LINE"
/note="Vector: Homo sapiens T CELLS (JURKAT CELL LINE)"
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.

```


Library was not normalized."

```
ORIGIN
Query Match      1.4%; Score 51.8; DB 5; Length 886;
Best Local Similarity 38.6%; Pred. No. 0.085;
Matches 118; Conservative 34; Mismatches 154; Indels 0; Gaps 0;

QY 1851 AATAAGTATAAGTAAATAGCAGGTAGACAAACGGTTTCACCTTTGATATAAAATGAATTCAT 1910
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 86 RAAAAAATAGGAAAWARREGGAGRABATGAAMWTTGAWAANGANNANNTAANNANG 145
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1911 TCAATATTGCAACTTCGAGACGAGATACGATTTAGAAAGGGCGCAGAGCGGTGAA 1970
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 146 GNAATATTACNNNTWCMWAAAGRAAARAGAAARAGAAARAGAAARAGAAATTAATAATWMC 205
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1971 TGCTCTGTTTACTTAATACCAATCCAGAGATTTGAAACAGATGTGACAGATTATCATAT 2030
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 206 TGAATATTGTCGAAATATWCAAGGAGGAAWAGAAATGGAACACACATMAAAA 265
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2031 TGATCAAGTATCCAAATTTAGTGGCGGTGTTTATCGGATGAAATCTCTGTAGATGAAAGAG 2090
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 266 AATDTADAADAADAADAKKDATATATWAAAAAAWAKATKAKATTTKGKAAGAAWAWAA 325
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2091 AGAATTACTTGAGAAAGTGAATATCGGAAACGACTCAGTGATGAAAGAACTTACTCCA 2150
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 326 TGGATGAWAWRAAAMAAARAAATAGAAWAAACCTATTWATTARAATARAAGARAAARAA 385
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2151 AGATCC 2156
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 386 AAAGCC 391
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
CNS00EVL      1101 bp      DNA      linear      GSS 04-JUN-1999
LOCUS         Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION    BACR2923 of RPCI-98 library from Drosophila melanogaster (fruit
              fly), genomic survey sequence.
ACCESSION     AL069706
VERSION       AL069706.1 GI:4949849
KEYWORDS      GSS.
SOURCE        Drosophila melanogaster (fruit fly)
ORGANISM      Drosophila melanogaster
              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Ephydroidea; Drosophilidae; Drosophila.
REFERENCE     1 (bases 1 to 1101)
              Genoscope.
              Direct Submission
              Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
              BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
COMMENT       Determination of this BAC-end sequence was carried out as part of a
              collaboration with the Berkeley Drosophila Genome Project (BDGP).
              The BDGP is constructing a physical map of the Drosophila
              melanogaster genome using these BACs. For further information
              please see http://www.fruitfly.org The BDGP Drosophila
              melanogaster BAC library was prepared by Kazutoyo Osoegawa and
              Aaron Mammosser in Pieter de Jong's laboratory in the Department of
              Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
              NY. The library is named RPCI-98 and was constructed by partial
              EcoRI digestion of Drosophila DNA provided by the BDGP from the
              isogenic strain y2; cn bw sp, the same strain used for the BDGP's
              P1 and EST libraries. A more detailed description of the library
              and how to order individual BAC clones, the entire library, or
              filters for hybridization from the BACPAC Resource Center can be
              found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES      Location/Qualifiers
              1..1101
                 /organism="Drosophila melanogaster"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:7227"
                 /clone="BACR2923"

/clone lib="RPCI-98"
/note="end : T7"

ORIGIN
Query Match      1.4%; Score 51.8; DB 9; Length 1101;
Best Local Similarity 33.3%; Pred. No. 0.09;
Matches 209; Conservative 96; Mismatches 318; Indels 4; Gaps 2;

QY 1851 AATAAGTATAAGTATAATGCGAGGTAGACAAACGGTTTCACCTTTGATATAAAATGAATTCAT 1910
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 470 WMAATWTTWAAAWAAAWTTTAAATWAAAAAAWAWWWATTTTTTWWWTWTTTWTWTW 529
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1911 TCCATTTACTGCAACCTTCGAGACGAGATACGATTTAGAAAGGGCGCAGAGCGGTGAA 1970
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 530 WTTWTAWTAATAAAAAAATAATTTTAAAWAAATAWATTAWAAATTTAAWAAWTTATATAT 589
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1971 TGCTCTGTTTACTTAATACGAAATCCAGAGATTTGAAACAGATGTGACAGATTATCATAT 2030
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 590 WTATAAATWTTWATTAATAATAAAAAAATATTTTTTWTATAAAATTTTAAATTAATTAATTAW 649
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2031 TGATCAAGTATCCAAATTTAGTGGCGGTGTTTATCGGATGAAATCTCTGTAGATGAAAGAG 2090
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 650 TTATTAAATAATWTTWTTAAATTAATAATTTWAAATWAAAAAATAAAAAAATAAAWATW 709
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2091 AGAATTACTTGAGAAAGTGAATATGCGAAACGACTCAGTGATGAAAGAACTTACTCCA 2150
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 710 AAWAATWATAWATAATTTAAAWAAATAAAWAAATAWAAWATATATATWATATATATWTT 769
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2151 AGATCCAAACTTCACATCCAT-CAATAAGCAACGAGCTTCATATCTACTTAATGAGCAAT 2209
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 770 WTAWWWATWAAWWWTATATAWATAWAAWAAWATAAAATAWATAWATAWAAWAAWAAWAT 829
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2210 CGAATTTTCACATCTATCCATGAACATCTGAACATGCGTGGGAGAGTGAGACATTA 2269
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 830 AWAATATATATAWAAATAWAAAAAATAWTAATAWTAATAWAAWAAAAAATAWATTTWTT 889
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2270 CAATCCGAGAAAGAAATGACCGTATTTTAAAGAGAAATTCAGTCACACTACCGGGGACTTTTA 2329
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 890 WTTTWWAAWATATAAAWAAWATAWAAWAAWAAAAAATAAAATAWAAWTTWATATTTTA 949
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2330 ATGAGTGTAT---CCGACGTTTATTTATCAAAAAATAGGAGAGTCGGAAATTTAAAGCTT 2386
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 950 TTAATAATWTTATWTTWTTWTTWTTWTTWTTWTTWTTWTTWTTWTTWTTWTTWTTWTT 1009
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2387 ATACTCGCTACCAATTAAGAGGTATATTGAAGATAGTCAAGATTTAGAGATATATTTGA 2446
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1010 TATTAAWTTATATTTTAAWAAWTTATATATATWATAWTTWATAWATAWAAWAAATTTATA 1069
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2447 TTCGTTATTAATGCGAAACATGAAACAT 2473
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1070 TATWATAWATAWAAWAAWAAWAAWAAWAT 1096
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
LOCUS         AZ549980
DEFINITION    ENTDD94TP Entamoeba histolytica Sheared DNA Entamoeba histolytica
              genomic, genomic survey sequence.
ACCESSION     AZ549980
VERSION       AZ549980.1 GI:11175122
KEYWORDS      GSS.
SOURCE        Entamoeba histolytica
ORGANISM      Entamoeba histolytica
              Eukaryota; Entamoebidae; Entamoeba.
REFERENCE     1 (bases 1 to 900)
              Loftus, B., Van Aken, S. and Fraser, C.
              Determination of clone end sequences from Entamoeba histolytica
              HMI:IMSS sheared DNA library
              Unpublished (2000)
              Contact: Brendan J Loftus
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
```

Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjloftus@tigr.org
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
 DNA library
 Seq primer: M13-Forward
 Class: shotgun
 High quality sequence start: 20
 High quality sequence stop: 890.
 Location/Qualifiers
 1..900
 /organism="Entamoeba histolytica"
 /mol_type="genomic DNA"
 /strain="HMI:IMSS"
 /db_xref="taxon:5759"
 /clone_lib="Entamoeba histolytica Sheared DNA"
 /note="Vector: pHOsi; Site 1: Bat I; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from broth cultures of E. histolytica
 using a method described by Clark and Diamond (Clark,
 C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
 method for isolate identification. Exp. Parasitol.
 77:450.). The DNA was mechanically sheared to give a
 tight size distribution (-2 kb). The v + i method used for
 the library construction is described in detail in Smith,
 H.O. and Venter, J.C. (Making small insert libraries for
 whole genome shotgun sequencing projects. In Genome
 Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Borell, Oxford University Press, 1999)."
 ORIGIN
 Query Match
 Best Local Similarity 1.4%; Score 51.2; DB 8; Length 900;
 Matches 146; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
 QY 3290 ATGAATCGAGAACATACAGACGAACTAAATTTTAAAACTGTGAGAGAGGAAGTGT 3349
 Db |||||
 QY 323 ATGAAGATGATGAAGATGATGAAGAGATGAGACGAGATGATGAAGACGATGAAG 382
 Db |||||
 QY 3350 ATCAACGATATACAGAACGCTGATGATGATGATGATGATGATGATGATGATGATG 3409
 Db |||||
 QY 383 ATGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 442
 Db |||||
 QY 3410 ATTCCCGTATCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3469
 Db |||||
 QY 443 AAGAAGATGAAGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 502
 Db |||||
 QY 3470 ACACACCGACTTATGAGACGACGATGATGATGATGATGATGATGATGATGATGATG 3529
 Db |||||
 QY 503 ATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGA 562
 Db |||||
 QY 3530 ATGACAGAGGTATGTGAATATTCACCACTACCACTGATGATGATGATGATGATGATG 3589
 Db |||||
 QY 563 ATGATGAAGATGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 622
 Db |||||
 QY 3590 AATA 3593
 Db |||||
 QY 623 AAGA 626

RESULT 12
 CNS00EMH/c
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence T7 end of BAC:
 BAC29M06 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL069378
 AL069378.1 GI:4949521
 GSS
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

REFERENCE AUTHORS TITLE JOURNAL

Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mamoser in Piter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial,
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the BDGP's
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

COMMENT

Location/Qualifiers

1..1101
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR29M06"
 /clone_lib="RPCI-98"
 /note="end : T7"

FEATURES source

Location/Qualifiers
 1..1101
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR29M06"
 /clone_lib="RPCI-98"
 /note="end : T7"

ORIGIN

Query Match
 Best Local Similarity 1.4%; Score 51; DB 9; Length 1101;
 Matches 102; Conservative 69; Mismatches 148; Indels 0; Gaps 0;
 QY 2681 CGGTGGTGGTGTATTCAGATTAAAGACGAGCAGGATCATGCAAGCTAGGGAATCTCG 2740
 Db |||||
 QY 932 GGGTGTGAGKWRATKRDWAKWTRWTAWAAWATATATATATATATATATATATATATAT 873
 Db |||||
 QY 2741 AATTATTGAAGAACCATTTATAGGAGAGCAGCTGTCTGTGTGAAGAGAGCAGAGA 2800
 Db |||||
 QY 872 AKTGATGAGRRARARAKGTGTATGATWAKAKAKAKKATGTGKAGATRTD 813
 Db |||||
 QY 2801 AAAAATGGAGACAAACGCGTGAACAACTACATTCGAAACAAACGATATATACAGAGG 2860
 Db |||||
 QY 812 AGACAGAGTRGRWAGTATATATRAARADAGATATAAGGDRATKARRAKATRTAGGA 753
 Db |||||
 QY 2861 CAAAAGAGCTGGATGCTTTTATTGTAGATTCTCAATATAATAGATTCAAGCGGATA 2920
 Db |||||
 QY 752 KRWAACAKWAGAGTGWAKAKATGTGWTATTTKAKWRKARKRWGTAKATDTTGRAAAA 693
 Db |||||
 QY 2921 CAACATTTGCGATGATTCATGCGCAGATAAATTTGTTTCATCGAATTCGAGAGCTTATC 2980
 Db |||||
 QY 692 AATAAAGAGATRTTRRRKRWKAWAWATATAAGTGTGAGAAAARAGAAAGTGTGTG 633
 Db |||||
 QY 2981 TGTCAGAAATTTATCTGTAT 2999
 Db |||||
 QY 632 TDGGGKKDKXTDGRWGT 614

RESULT 13 AG280055/c

LOCUS

DEFINITION

Mus musculus molossinus DNA, clone:MSM01-051D13.T7, genomic survey

ACCESSION

AG280055

VERSION

AG280055.1

KEYWORDS

GSS.

SOURCE

Mus musculus molossinus

ORGANISM

Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE	1	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
AUTHORS		BAC and Sequences of Library MSMg01
TITLE	2	(bases 1 to 1337)
REFERENCE	2	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
AUTHORS		Direct Submission
TITLE		Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
JOURNAL		and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
		1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
		(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/ ,
		Tel: 81-45-503-9111, Fax: 81-45-503-9170)
		Clones are derived from the mouse BAC library MSMg01. For BAC
		library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
		The Institute of Physical and Chemical Research (RIKEN) 3-1-1
		Tsukuba Institute, Bio Resource Center,
		Koyadai, Tsukuba, 305-0074 Japan
		phone: 81-298-36-9189, fax: 81-298-36-9199
		e-mail: abe@rtc.riken.jp
COMMENT		

FEATURES
SOURCE

```

1. 912
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/notes="Vector: pHO31; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
C.G. for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v+1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

```

ORIGIN

Query Match	1.4%;	Score 50.6;	DB 8;	Length 912;
Best Local Similarity	42.7%;	Pred. No. 0.17;		
Matches 260;	Conservative	0;	Mismatches 349;	Indels 0; Gaps 0;
3007	GTAAATGCGGAAATTTTGAAGAATTAGAAAGGTGCGCATTTATCACTCGCAATCTCCCTATAC	3066		
243	GAAGATGATGAAGATGATGATGATGAAGAAGATGATGATGAAGAAGATGATGATGAAGAA	302		
3067	GATGCGAGAAATGCTCGTTAAAAATGCTGATTTTAAATAATGAGTATAGCATGCTCGGAATGTA	3126		
303	GATGATGATGATGAAGAAGATGATGAAGAAGATGATGAAGAAGAAAGATGATGAAGAT	362		
3127	AAAGGSCATGTAGATGTCAACACAGAGCCATCACCGTTCTGCTCTCTTATCCACAGATCG	3186		
363	GAAGATGATGAAGCATGTGACGACGACGATATGAATTTAGAAGATGATGATGAAGAA	422		
3187	GAAGCAGAAAGTGTCAACACAGTGTGCGCTGTGTCCGGGCGTGGCTATATCTCCGTGTC	3246		
423	GAAGAAGATGATGATGAAGATGATGAAGACGATGAAGACGACGAATATGAATTAGAAGAT	482		
3247	ACAGCGTACAAAGAGGGATATCGAGAGGGTGTGTAAACGATCCATGAAATCGAGAACAAAT	3306		
483	GATGATGATGATGAAGAAGATGATGATGAAGAAGAAGATGATGATGAAGATGAT	542		
3307	ACAGACGAACTAAAAATTTAAAAACTGTGTGAAGAAGAGGAAGTGTATCCACGGGATACAGGA	3366		
543	GATGAAGAAGAAGATGAAGAAGATGATGAAGAAGATGATGAAGAAGATGATGAAGAAGAA	602		
3367	ACGTGTAATGATTATCTGCCACCAAGGTACAGCAGTATGTAATTCCTCCGTATGCTGGA	3426		
603	GAAGATGATGATGAAGATGATGAAGACGATGAAGACGACGAATATGAATTTAGAAGATGAT	662		
3427	TATGAGGATGCATATGAAGTTGATACTACAGCATCTGTTAAATTTACAAACCGACTTATGAA	3486		

RESULT 14	AZ551092	912 bp	DNA	linear	GSS 14-NOV-2000
LOCUS	AZ551092				
DEFINITION	ENTFE222F Entamoeba histolytica Sheared DNA				Entamoeba histolytica
ACCESSION	AZ551092				genomic, genomic survey sequence.
VERSION	AZ551092.1				GI:11176393
KEYWORDS	GSS.				
SOURCE	Entamoeba histolytica				
ORGANISM	Entamoeba histolytica				
	Eukaryota; Entamoebidae; Entamoeba.				

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2004, 13:33:31 ; Search time 119 Seconds
(without alignments)
3701.845 Million cell updates/sec

Title: US-10-614-524-2

Perfect score: 6479

Sequence: 1 LTSNRKNEINIALSIPAV.....ICETEGKFIVDSVEILLMEE 1228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6479	100.0	1228	4	AAB84628 Amino aci
2	6462	99.7	1228	4	Aau02039 B. thurin
3	5926.5	91.5	1227	2	Aaw44321 Bacillus
4	5926.5	91.5	1227	4	Aab19950 Bacillus
5	5912.5	91.3	1227	4	Aau02046 B. thurin
6	5740	88.6	1228	2	Aar50955 Bacillus
7	5436.5	83.9	1227	2	Aay31990 Chimeric
8	5237.5	80.8	1229	2	Aar54074 CryET5. 2
9	5237.5	80.8	1229	2	Aaw35259 Bacillus
10	5237.5	80.8	1229	2	Aaw17699 CryET5. 3
11	5237.5	80.8	1229	2	Aaw87633 CryET5 pr
12	5237.5	80.8	1229	2	Aay30923 B. thurin
13	5237.5	80.8	1229	8	Adk98479 B thuring
14	5233.5	80.8	1230	8	Adk98484 B thuring
15	5233.5	80.8	1230	8	Adk98489 B thuring
16	5233.5	80.8	1230	8	Adk98481 B thuring
17	5233.5	80.8	1230	8	Adk98491 B thuring
18	5233.5	80.8	1230	8	Adk98487 B thuring
19	5189.5	80.1	1209	4	Aau02094 Bacillus
20	5183.5	80.0	1221	4	Aau00421 B. thurin
21	5169.5	79.8	1221	4	Aau00420 B. thurin
22	5108	78.8	1186	2	Aay16796 Amino aci
23	4791	73.9	1208	4	Aau02093 Bacillus
24	4303.5	66.4	1217	4	Aau02092 Bacillus
25	3977.5	61.4	1174	2	Aar89494 B.t. toxi

26	3977.5	61.4	1174	2	AAW09043	Aaw09043 Bacillus
27	3974.5	61.3	1174	2	AAR25825	Aar25825 Novel tox
28	3969.5	61.3	1174	2	AAR08257	Aar08257 B.thuring
29	3791	58.5	1176	2	AAW46737	Aaw46737 Amino aci
30	3791	58.5	1176	2	AAW47035	Aaw47035 Bacillus
31	3579	55.2	1170	2	AAR63231	Aar63231 Cryetal p
32	3556	54.9	1167	2	AAW54073	Aar54073 CryET4. 2
33	3556	54.9	1167	2	AAW35258	Aaw35258 Bacillus
34	3556	54.9	1167	2	AAW17700	Aaw17700 CryET4. 3
35	3556	54.9	1167	2	AAW87632	Aaw87632 CryET4 pr
36	3556	54.9	1167	2	AAW30922	Aaw30922 B. thurin
37	3502.5	54.1	1189	2	AAW61345	Aaw61345 a mutated
38	3502.5	54.1	1189	2	AAW17783	Aay17783 EGI2111 c
39	3502.5	54.1	1189	3	AAW82431	Aay82431 Bacillus
40	3502.5	54.1	1189	5	AAE26471	Aae26471 Bacillus
41	3502.5	54.1	1189	5	ABG93849	Abg93849 B. thurin
42	3502.5	54.1	1189	7	ABW02350	Abw02350 B. thurin
43	3500.5	54.0	1189	2	AAW61335	Aaw61335 A mutated
44	3500.5	54.0	1189	2	AAW17788	Aay17788 B. thurin
45	3500.5	54.0	1189	3	AAW82396	Aay82396 Bacillus

ALIGNMENTS

RESULT 1

AAB84628
ID AAB84628 standard; protein; 1228 AA.

XX AC AAB84628;

XX DT 05-SEP-2001 (first entry)

XX DE Amino acid sequence of a CryIBf insecticidal protein.

XX KW CryIBf; insecticidal protein; CryIJd; Cry9Fa; lepidoptera; coleoptera;
insect pest; transgenic plant.

XX OS Bacillus thuringiensis.

XX PN WO000147952-A2.

XX PD 05-JUL-2001.

XX PF 19-DEC-2000; 2000WO-EP013184.

XX PR 28-DEC-1999; 99US-0173387P.

XX PA (AVET) AVENTIS CROPS SCIENCE NV.

XX PI Arnaut G, Boets A, Damme N, Mathieu E, Vanneste S, Van Rie J;

XX DR WPI; 2001-425619/45.

XX DR N-PSDB; AAB28240.

XX PT Novel insecticidal proteins CryIJd, Cry9Fa and CryIBf, derived from
Bacillus thuringiensis, useful for controlling insects in plants.

XX PS Claim 11; Page 37-41; 65pp; English.

XX CC The present sequence represents CryIBf, an insecticidal protein derived
from Bacillus thuringiensis. The specification also describes CryIJd and
Cry9Fa. The Cry proteins have activity against lepidopteran and
coleopteran insect pests. CryIBf, CryIJd and Cry9Fa polynucleotides and
Cry polypeptides are useful for obtaining a plant with resistance to insects.
Cry polynucleotides are useful for producing transgenic plants which are
resistant to insects

XX SQ Sequence 1228 AA;

Query Match 100.0%; Score 6479; DB 4; Length 1228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTSNRKXENEIINALSIPAVSNHSTQMDLSDPARIEDSLCIAAGNNINPLVSASTVQTGI 60
Db 1 LTSNRKXENEIINALSIPAVSNHSTQMDLSDPARIEDSLCIAAGNNINPLVSASTVQTGI 60
QY 61 NIAGRILGVLGVPPFAQGIASFYSFLVGLWPRGRDQWEIFLEHVBLINQOITENARNTA 120
Db 61 NIAGRILGVLGVPPFAQGIASFYSFLVGLWPRGRDQWEIFLEHVBLINQOITENARNTA 120
QY 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLTQYIALELDFLNAAMPLFAIRNQEV 180
Db 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLTQYIALELDFLNAAMPLFAIRNQEV 180
QY 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQIEIQRYEROVEQTRDYSDYCVWYNTGLN 240
Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQIEIQRYEROVEQTRDYSDYCVWYNTGLN 240
QY 241 SLRGTTAAASWRYNQFRRLDLTLGLVDLVALFPFSDYDTRTYPINTSAQLTREYVTDAGTG 300
Db 241 SLRGTTAAASWRYNQFRRLDLTLGLVDLVALFPFSDYDTRTYPINTSAQLTREYVTDAGTG 300
QY 301 VMASMMWYNNAPSFAIETAVITRSPLHLDLFLQLTIPFSTSSRWASATRHMTYWRGHTIQ 360
Db 301 VMASMMWYNNAPSFAIETAVITRSPLHLDLFLQLTIPFSTSSRWASATRHMTYWRGHTIQ 360
QY 361 SRPIGGGLTSTHGSTNTSINPVRLSFFSRDVTWYTESYAGVLLWGIYLEPIHGVPTVRFN 420
Db 361 SRPIGGGLTSTHGSTNTSINPVRLSFFSRDVTWYTESYAGVLLWGIYLEPIHGVPTVRFN 420
QY 421 FRNPQNTFERGTANYSQYPSFGLQKDSETELPETTERPNYESYSHRSLHGLISQSR 480
Db 421 FRNPQNTFERGTANYSQYPSFGLQKDSETELPETTERPNYESYSHRSLHGLISQSR 480
QY 481 VHVPIYSWTHRSADRTNTISSDSTQIPLVKSFNLSNGTSVUSGPGTGGDIIRTNVNGS 540
Db 481 VHVPIYSWTHRSADRTNTISSDSTQIPLVKSFNLSNGTSVUSGPGTGGDIIRTNVNGS 540
QY 541 VLSGLNPNNTSLQRYRVRYAAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQSPR 600
Db 541 VLSGLNPNNTSLQRYRVRYAAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQSPR 600
QY 601 PAEPFVGISAGSGTAGISISNNAGROTFFHDKIEFIPITATFEAEYDLEAQAENALF 660
Db 601 PAEPFVGISAGSGTAGISISNNAGROTFFHDKIEFIPITATFEAEYDLEAQAENALF 660
QY 661 TINTNPRLKTDDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPN 720
Db 661 TINTNPRLKTDDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPN 720
QY 721 FTSINKQPDFTISTNEQSNFTSIHQSEHGHWGSENITIOEGNDVPKENYVTLPGTFNECY 780
Db 721 FTSINKQPDFTISTNEQSNFTSIHQSEHGHWGSENITIOEGNDVPKENYVTLPGTFNECY 780
QY 781 PTLYLYQIGSELSKAYTRYQLRGVIEDSQDLEIYLIRYNKAKHETLDVPGTESWPLSVES 840
Db 781 PTLYLYQIGSELSKAYTRYQLRGVIEDSQDLEIYLIRYNKAKHETLDVPGTESWPLSVES 840
QY 841 PIGRCGEPNRCAPHFENPDLDCSRDGEKCAHSHHFSIDIDIGCTDLHENLGVWVVKF 900
Db 841 PIGRCGEPNRCAPHFENPDLDCSRDGEKCAHSHHFSIDIDIGCTDLHENLGVWVVKF 900
QY 901 IKTOEGHARLGNLEFTEEPKLLGEALSRVKRAEKWRDKREKLQLETKRYVTEAKEAVDA 960
Db 901 IKTOEGHARLGNLEFTEEPKLLGEALSRVKRAEKWRDKREKLQLETKRYVTEAKEAVDA 960
QY 961 LFVDSQYNRLQADTNIGMHAADKLVHRIREAYLSLSVPGVNAIRIPEELSGRIITALS 1020
Db 961 LFVDSQYNRLQADTNIGMHAADKLVHRIREAYLSLSVPGVNAIRIPEELSGRIITALS 1020
QY 1021 LYDARNVKNKGNDFNGLACWNVKGVHDVQOSSHRSVLVTPWEAEVSQAVRVCPCRGVIL 1080
Db 1021 LYDARNVKNKGNDFNGLACWNVKGVHDVQOSSHRSVLVTPWEAEVSQAVRVCPCRGVIL 1080

QY 1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKNCBEEVYPTDTGTCNDYTAHQGTAVCNERN 1140
Db 1081 RVTAYKEGYGEGCVTIHEIENNTDELKFKNCBEEVYPTDTGTCNDYTAHQGTAVCNERN 1140
QY 1141 AGYEDAYEVDTTASVNYKPTYEETVTVRRDNHCEYDRGVYVNPPLPAGYMTKELEYFP 1200
Db 1141 AGYEDAYEVDTTASVNYKPTYEETVTVRRDNHCEYDRGVYVNPPLPAGYMTKELEYFP 1200
QY 1201 ETDKWIIEIGETEGKFIVDSVLELLMEE 1228
Db 1201 ETDKWIIEIGETEGKFIVDSVLELLMEE 1228
RESULT 2
AAU02039
ID AAU02039 standard; protein; 1228 AA.
XX AAU02039;
XX 29-AUG-2001 (first entry)
XX B. thuringiensis toxic crystal protein, CryET64.
DE Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
XX transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
XX sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
XX pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
XX cactus; tree call; gypsy moth; looper; tobacco budworm; spruce budworm;
XX cotton leaf perforator; CryET64.
OS Bacillus thuringiensis.
XX
XX WO200119859-A2.
XX 22-MAR-2001.
XX 13-SEP-2000; 2000WO-US025361.
XX 15-SEP-1999; 99US-0153999SP.
XX (MONS) MONSANTO CO.
XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
XX WPI: 2001-281518/29.
XX N-PSDB; AAS02482.
PT Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
PT and the polynucleotides that encode them, useful for increasing the
XX insect resistance of plant.
XX
XX Claim 5; Page 139-141; 173pp; English.
XX
XX The sequence represents a B. thuringiensis Lepidopteran-active delta-
XX endotoxin, crystal protein CryET64. The Lepidopteran-active B.
XX thuringiensis delta-endotoxin polypeptides may be used as compositions
XX that are applied to plant crops to protect them from insect damage. The
XX polynucleotides may be used in the production of transgenic plants that
XX express the insecticidal polypeptides and consequently have improved
XX insect resistance compared to non-transformed plants. Monocotyledonous or
XX dicotyledonous plants may be protected in this way, for example corn,
XX wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
XX tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
XX fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
XX cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
XX cotton leaf perforator and spruce budworm) may be affected by application
XX of the insecticidal polypeptides (full details given in specification)
SQ Sequence 1228 AA;

Query Match 99.7%; Score 6462; DB 4; Length 1228;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1223; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTSNRKNEINEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db :
QY 1 MTSNRKNEINEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
61 NIAGRIILGVLGVPFAGIATASFSPLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
Db 61 NIAGRIILGVLGVPFAGIATASFSPLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
QY 121 LARLOGLGDSFRAYQOQSLDLEWLNEDDARTSVLTYQVIALELDFLNAMPLFAIRNQVVP 180
Db 121 LARLOGLGDSFRAYQOQSLDLEWLNEDDARTSVLTYQVIALELDFLNAMPLFAIRNQVVP 180
QY 181 LMVYAQAANTHLLLRDASLFGSFGSLTSQBIQRYERQVEQTRDYSYDQVWNTGLN 240
Db 181 LMVYAQAANTHLLLRDASLFGSFGSLTSQBIQRYERQVEQTRDYSYDQVWNTGLN 240
QY 241 SURGTNAASWVRYNQFRDLTLGVLDLVALPFSYDTRTPINTSAQLTREVTDAIGATG 300
Db 241 SURGTNAASWVRYNQFRDLTLGVLDLVALPFSYDTRTPINTSAQLTREVTDAIGATG 300
QY 301 VNMASSMNWNNAPSFSAIETAVIRSPHLLDLEQLTIFSTSSRSASATRHMTYWRGHTIQ 360
Db 301 VNMASSMNWNNAPSFSAIETAVIRSPHLLDLEQLTIFSTSSRSASATRHMTYWRGHTIQ 360
QY 361 SRPICGGLNTSTHGSTNTSINPVLSPFSRDVYMTESYAGVLLMGILYLEPIHGVPTVRPN 420
Db 361 SRPICGGLNTSTHGSTNTSINPVLSPFSRDVYMTESYAGVLLMGILYLEPIHGVPTVRPN 420
QY 421 FRNPQNTFERGTANTSQPYESPGLQIKDSETELPETTERPNYESYSHRLSHIGLISQSR 480
Db 421 FRNPQNTFERGTANTSQPYESPGLQIKDSETELPETTERPNYESYSHRLSHIGLISQSR 480
QY 481 VHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVGPGFTGGDIIRNVNGS 540
Db 481 VHVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGTSVVGPGFTGGDIIRNVNGS 540
QY 541 VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPTSMANESLTSQSPR 600
Db 541 VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVTVGGSTTFDQGFPTSMANESLTSQSPR 600
QY 601 FAEPPVGISASGSGTAGISINNAGROTFHFKIEFIPITATFEAYDLERAQEAVALNF 660
Db 601 FAEPPVGISASGSGTAGISINNAGROTFHFKIEFIPITATFEAYDLERAQEAVALNF 660
QY 661 TTNTPRLKTDVTDHIDQVSNLVAQLSDFECLDEKRELLKVKYAKRLSDERNLQDPN 720
Db 661 TTNTPRLKTDVTDHIDQVSNLVAQLSDFECLDEKRELLKVKYAKRLSDERNLQDPN 720
QY 721 FTSINKQPDFISTNEQSNFTSIEHQSEHGWSGSENITIQEGNDVPKENYVTLPGTFNECY 780
Db 721 FTSINKQPDFISTNEQSNFTSIEHQSEHGWSGSENITIQEGNDVPKENYVTLPGTFNECY 780
QY 781 PTYLQKIGESLKAYTRYQLRGYIEDSQDLBIYLIRYNAKHETLDVPGTSEWPLSVES 840
Db 781 PTYLQKIGESLKAYTRYQLRGYIEDSQDLBIYLIRYNAKHETLDVPGTSEWPLSVES 840
QY 841 PIKRGCEPNRCAPHEPWPDLDCSDGCKCAHSHHPSLSDIDIGCTDLHENLGVWVFK 900
Db 841 PIKRGCEPNRCAPHEPWPDLDCSDGCKCAHSHHPSLSDIDIGCTDLHENLGVWVFK 900
QY 901 INTQEGHARLGNLEFIEEKPLLGEALSRYKRAEKKWRDKREKQLETKRVYTEAKEAADA 960
Db 901 INTQEGHARLGNLEFIEEKPLLGEALSRYKRAEKKWRDKREKQLETKRVYTEAKEAADA 960
QY 961 LFPVDSQYNRLQADTNIGMITHAADKLVRHIREAYLSLSELSVIPGVNAIEFEELEGRIITAIS 1020
Db 961 LFPVDSQYNRLQADTNIGMITHAADKLVRHIREAYLSLSELSVIPGVNAIEFEELEGRIITAIS 1020
QY 1021 LYDARNVKNKGDFNNGLCANWVKGVHVDVQOSSHRSVLVITPEWEAEVSQAVRVCPCRGYIL 1080
Db 1021 LYDARNVKNKGDFNNGLCANWVKGVHVDVQOSSHRSVLVITPEWEAEVSQAVRVCPCRGYIL 1080

QY 1081 RVTAYKEGYGCGCVTIHIEINNNTDELKPKNCEEBEVYPTDTGTCNDYTAHQGTAVCNERN 1140
Db 1081 RVTAYKEGYGCGCVTIHIEINNNTDELKPKNCEEBEVYPTDTGTCNDYTAHQGTAVCNERN 1140
QY 1141 AGYEDAVEVDVTASVNYKPTVEEETDVRDHNCEYDRGVYVNPPLPAGYMTKELEYPP 1200
Db 1141 AGYEDAVEVDVTASVNYKPTVEEETDVRDHNCEYDRGVYVNPPLPAGYMTKELEYPP 1200
QY 1201 ETDKVMWIEIGETEGKFIVDSVELLIMEE 1228
Db 1201 ETDKVMWIEIGETEGKFIVDSIELLIMEE 1228
RESULT 3
AAW44321
ID AAW44321 standard; protein; 1227 AA.
XX
AC AAW44321;
XX
DT 27-MAY-1998 (first entry)
XX
DE Bacillus thuringiensis 158C2c toxin.
XX
KW Bacillus thuringiensis; 158C2c; toxin; lepidopteran-active; insect;
KW microbe; transgenic plant; resistant.
XX
OS Bacillus thuringiensis.
XX
PN USS723758-A.
XX
PD 03-MAR-1998.
XX
PF 23-MAY-1995; 95US-00448170.
XX
PR 13-SEP-1991; 91US-00759247.
PR 01-JUN-1993; 93US-00069902.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Stelman S, Narva KE, Cummings DA, Payne J, Cannon RJ;
PI WPI; 1998-178600/16.
DR N-PSDB; AAV15222.
XX
PT DNA encoding Bacillus thuringiensis toxin proteins - for producing
transgenic plants resistant to attack by lepidopteran pests.
XX
PS Claim 1; Col 33-40; 25pp; English.
XX
CC The present sequence represents a 158C2c toxin from Bacillus
thuringiensis. The present invention describes isolated nucleic acid
sequences encoding toxins active against lepidopteran insects. The
present invention also describes a recombinant host transformed with a
nucleic acid sequence encoding a toxin. The nucleic acid sequence can be
amplified. The product is used for producing transgenic plants resistant
to attack by lepidopteran pests. N.B. The numbers in the sequence listing
do not correspond to the SEQ ID NO.'s mentioned in the specification e.g.
in the specification SEQ ID NO:3, 4, 5 and 6 are said to correspond to
the nucleic acid sequences encoding the toxins, and SEQ ID NO:7, 8, 9 and
10 are said to correspond to the amino acid sequences of the toxins,
whereas in the sequence listing the amino acid sequence is given after
the nucleic acid sequence encoding it (i.e. SEQ ID NO:3 encodes SEQ ID
NO:4)
XX
SQ Sequence 1227 AA;
Query Match 91.5%; Score 5926.5; DB 2; Length 1227;
Best Local Similarity 91.8%; Pred. NO. 0;
Matches 1129; Conservative 36; Mismatches 60; Indels 5; Gaps 3;
QY 1 LTSNRKNEINEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db 1 LTSNRKNEINEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNIDPFVSASTVQTGI 60


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QY 181 LLAVYAAQANLHLLLRDASLFGSEFGLTSQBIQRYERQVEQTRDYSQVCVWYNTGLN 240
Db 181 LLAVYAAQANLHLLLRDASLFGSEFGLTSQBIQRYERQVEQTRDYSQVCVWYNTGLN 240
QY 241 SLRGNTAAASWRYNQRDLTLGVLDLVALPSSYDTRTPINTSAQLTRVTVDAIGATG 300
Db 241 SLRGNTAAASWRYNQRDLTLGVLDLVALPSSYDTRTPINTSAQLTRVTVDAIGATG 300
QY 301 V--NMASMMWYNNAPSAIETAVIRSPHLDLFLQLTIFSTSSRWASATRMVYRGRHT 358
Db 301 V--NMASMMWYNNAPSAIETAVIRSPHLDLFLQLTIFSTSSRWASATRMVYRGRHT 358
QY 359 IQRPIGGGLNTSTHGSTNTSINPVLSFSDRVYMTESYAGVLWGIYLEPIHGVTVR 418
Db 359 IQRPIGGGLNTSTHGSTNTSINPVLSFSDRVYMTESYAGVLWGIYLEPIHGVTVR 418
QY 419 ENFRPNQPTFERGTANYSPQYSPGLQXDSLTELPPETTERPNYESYSHRLSHGLISQ 478
Db 419 ENFRPNQPTFERGTANYSPQYSPGLQXDSLTELPPETTERPNYESYSHRLSHGLISQ 478
QY 478 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSNFNLNSGTSVSGPGFTGGDIIRTNVN 537
Db 478 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSNFNLNSGTSVSGPGFTGGDIIRTNVN 537
QY 539 GSVLSMGLNFNNTSLQRYVRVRYAASQTMVLRTVVGSGTTTDFQGPPTMSANESLTSQS 598
Db 539 GSVLSMGLNFNNTSLQRYVRVRYAASQTMVLRTVVGSGTTTDFQGPPTMSANESLTSQS 598
QY 598 PFAPFPVGISAGSGTAGISISNNAGROTFFHDKIEFIPITATPEAEYDLERAQAVNA 658
Db 598 PFAPFPVGISAGSGTAGISISNNAGROTFFHDKIEFIPITATPEAEYDLERAQAVNA 658
QY 658 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELLEKVKYAKRLSDERNLLQD 718
Db 658 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCLDEKRELLEKVKYAKRLSDERNLLQD 718
QY 719 PNFTSINKQDPFISTNEQSNFTSIHQSEHGWSGSENITIQEGNDVFKENYVILPGTFNE 777
Db 719 PNFTSINKQDPFISTNEQSNFTSIHQSEHGWSGSENITIQEGNDVFKENYVILPGTFNE 777
QY 778 CYPTLYQKIGSELKAYTRYQIRGVIEDSDLEIYLIRYNAKHETLDVPGTESVWPLSV 838
Db 778 CYPTLYQKIGSELKAYTRYQIRGVIEDSDLEIYLIRYNAKHETLDVPGTESVWPLSV 838
QY 839 ESPICRCEPNRCAPHFENWPLDSCDRGKCAHSHHFLSIDIDIGCTDLHENLGVWVY 898
Db 839 ESPICRCEPNRCAPHFENWPLDSCDRGKCAHSHHFLSIDIDIGCTDLHENLGVWVY 898
QY 898 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVRAEKKWRDKREKLQLETKRVYTEAEV 957
Db 898 FKIKTQEGHARLGNLEFIEEKPLLGEALSRVRAEKKWRDKREKLQLETKRVYTEAEV 957
QY 958 DALFVDSQYRDLQADTNGIMHAADKLVRHIREAYLSELVTPGVNAIFEELEGRITTA 1017
Db 958 DALFVDSQYRDLQADTNGIMHAADKLVRHIREAYLSELVTPGVNAIFEELEGRITTA 1017
QY 1019 ISLYDARNVKNKGFNNGLACWNVKGVHDVQSHRSVLVPEWAEVSOAVRVCPCRGY 1078
Db 1019 ISLYDARNVKNKGFNNGLACWNVKGVHDVQSHRSVLVPEWAEVSOAVRVCPCRGY 1078
QY 1078 ILRVTAKEGYGEGCVTTHIEENNTDELKFNCEEEVYPTDTGTCNDYTAHQGTAVCN 1138
Db 1078 ILRVTAKEGYGEGCVTTHIEENNTDELKFNCEEEVYPTDTGTCNDYTAHQGTAVCN 1138
QY 1138 RNAGVEDAYEVDVTTASVNYKPYEETVYDVRDNHCEYDRGVNYVPLPAGYMTKELEY 1197
Db 1138 RNAGVEDAYEVDVTTASVNYKPYEETVYDVRDNHCEYDRGVNYVPLPAGYMTKELEY 1197
QY 1199 PPETDKVWIEIGETGKFTVDSVELLMEE 1228
Db 1199 PPETDKVWIEIGETGKFTVDSVELLMEE 1227
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RESULT 5

```
AAU02046
XX AAU02046 standard; protein; 1227 AA.
AC AAU02046;
XX 29-AUG-2001 (first entry)
XX B. thuringiensis toxic crystal protein, CryET54.
DE Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; sorghum;
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
KW cotton leaf perforator; CryET54.
XX
XX Bacillus thuringiensis.
OS WO200119859-A2.
XX 22-MAR-2001.
XX 13-SEP-2000; 2000WO-US025361.
XX 15-SEP-1999; 99US-0153995P.
XX (MONS ) MONSANTO CO.
XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
XX WPI; 2001-281518/29.
XX N-PSDB; AAS02489.
XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
and the polynucleotides that encode them, useful for increasing the
insect resistance of plant.
XX Claim 17; Page 169-173; 173pp; English.
XX The sequence represents B. thuringiensis Lepidopteran-active delta-
endotoxin, crystal protein CryET54. The Lepidopteran-active B.
thuringiensis delta-endotoxin polypeptides may be used as compositions
that are applied to plant crops to protect them from insect damage. The
polynucleotides may be used in the production of transgenic plants that
express the insecticidal polypeptides and consequently have improved
insect resistance compared to non-transformed plants. Monocotyledonous or
dicotyledonous plants may be protected in this way, for example corn,
tobacco, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
fruit, legume, vegetable, ornamental plant shrub, cactus and/or tree
cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
cotton leaf perforator and spruce budworm) may be affected by application
of the insecticidal polypeptides (full details given in specification).
CC Note: The present sequence does not have a cryET number assigned
explicitly in the specification, cryET54 (see table 5, page 56) is not
assigned to any Seq.ID number, the indexer has matched the spare sequence
to the spare cryET number, which may be incorrect
XX
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Sequence 1227 AA;

```
Query Match 91.3%; Score 5912.5; DB 4; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1127; Conservative 36; Mismatches 62; Indels 5; Gaps 3;
QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPARIEDSLCIAEGNNIDPFVSASTVQTGI 60
QY 61 NIAGRIILGVLPFAGQIASFYSFLVGLWELWPRGRDOWEIFLEHVEQLINQITENARNTA 120
Db 61 NIAGRIILGVLPFAGQIASFYSFLVGLWELWPRGRDOWEIFLEHVEHLRQOVTENTROTA 120
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QY 121 LARLOGLGDSFRAYQQSLEDWLENRRDARTSRVLYTQYIALELDPLNAMPLFAIRNQVVP 180
Db 121 LARLOGLGNSFRAYQQSLEDWLENRRDARTSRVLYTQYIALELDPLNAMPLFAIRNQVVP 180
QY 181 LLMVYAQAANLHLLLRDLASLFGSEFGLTSQEIQRYYERQVQEQTRDYSYCVVWYNTGLN 240
Db 181 LLMVYAQAANLHLLLRDLASLFGSEFGLTSQEIQRYYERQVQEQTRDYSYCVVWYNTGLN 240
QY 241 SLRGTTNAASWVRNQFRDLITGLVDLVALFSPYDTRTPINTSAQLTREYVTDIGRTN 300
Db 241 NLRGTTNAESWVRNQFRDLITGLVDLVALFSPYDTRTPINTSAQLTREYVTDIGRTN 300
QY 301 V--NMASMNWYNNAPSFSAIETAVIRSPHLADFEQLTIPSTSRWATRHMTYWRGHT 358
Db 301 APSGFASFTWNNAPSFSAIETAVIRSPHLADFEQLTIPSTSRWATRHMTYWRGHT 358
QY 359 IQSRPTGGGINTSTGNTSINPVLGFFSRDVTWYTESYAGVLLWGIYPIPIHGVPTVR 418
Db 361 LESRTIRGSLSTWTHGNTSINPVLGFFSRDVTWYTESYAGVLLWGIYPIPIHGVPTVR 418
QY 419 FNRFRPONTFERGTANYQSPYESGLOLKDSETELPPETTERPNYESYSHRLSHIGLISQ 478
Db 419 FNRWPLNSL-RGSLYITGYTGVGTQLFDSETELPPETTERPNYESYSHRLSHIRLISG 477
QY 479 SRVHVPTVSWTHRSADRTNTISSDSITQIPLVKSFNLSNGTSVVGPGFTGCDIIRTNVN 538
Db 478 NTLRAPVTVSWTHRSADRTNTISSDSITQIPLVKSFNLSNGTSVVGPGFTGCDIIRTNVN 537
QY 539 GSVLSMGLNFNNTSIQRVVRVRYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQS 598
Db 538 GSVLSMGLNFNNTSIQRVVRVRYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQS 597
QY 599 FRPAEFPVGISASGSQTAGISINNAGROTTFHDKIRFIPITATFEAYDLERAQEAUNA 658
Db 598 FRPAEFPVGISASGSQTAGISINNAGROTTFHDKIRFIPITATFEAYDLERAQEAUNA 657
QY 659 LFTNTNPRRLKTDVTDYHIDOVSNLVACLSDPECLDEKRELLEKVKYAKRLSDERNLLQD 718
Db 658 LFTNTNPRRLKTDVTDYHIDOVSNLVACLSDPECLDEKRELLEKVKYAKRLSDERNLLQD 717
QY 719 PNFTSINKQPPFISTNEOSNFTSHEQSEHGWSGSENIITTOEGNDVFKENYVTLPGTFNE 778
Db 718 PNFTSINKQPPFNNSGNSNFTSHEQSEHGWSGSENIITTOEGNDVFKENYVTLPGTFNE 777
QY 779 CYPYLYOKIGESLKYATRYQLRGYIEDSQDLIELYIRYNAXHETLDVPGTESVWPLSV 838
Db 778 CYPYLYOKIGESLKYATRYQLRGYIEDSQDLIELYIRYNAXHETLDVPGTESVWPLSV 837
QY 839 ESPIGRCQPNRCAPHFENWPDLDSCSDGCKCANHSHHPSLDIDIGCTDLHENLGVWV 898
Db 838 ESPIGRCQPNRCAPHFENWPDLDSCSDGCKCANHSHHPSLDIDIGCTDLHENLGVWV 897
QY 899 FKIQTOGHARLGNLEFIEBKPLIGALSRLVKAQKWRDKREKLOLETRVVTYEAKEAV 958
Db 898 FKIQTOGHARLGNLEFIEBKPLIGALSRLVKAQKWRDKREKLOLETRVVTYEAKEAV 957
QY 959 DALFVDSQYNRLQADTNIGIMHAADKLVRIRREAYLSLSVIPGVNAEIEFELEGRIITA 1018
Db 958 DALFVDSQYNRLQADTNIGIMHAADKLVRIRREAYLSLSVIPGVNAEIEFELEGRIITA 1017
QY 1019 ISLYDARNVVKNGDFNGLACWNVKGVHDVQQSHRSVLVPIPEWEAEVQAVRVCPCRGY 1078
Db 1018 ISLYDARNVVKNGDFNGLACWNVKGVHDVQQSHRSVLVPIPEWEAEVQAVRVCPCRGY 1077
QY 1079 ILRVATYKEGYGCGCVTHIEENNTDELKPKNCEEEVYPTDTGTCNDYTAHQGTAVCNS 1138
Db 1078 ILRVATYKEGYGCGCVTHIEENNTDELKPKNCEEEVYPTDTGTCNDYTAHQGTAVCNS 1137
QY 1139 RNAGYEDAVBDVTASVNVKPTVEETTYTDVRDNHCEYDRGVYVNPPLPAGYMTKELEY 1198
Db 1138 RNAGYEDAVBDVTASVNVKPTVEETTYTDVRDNHCEYDRGVYVNPPLPAGYMTKELEY 1197
QY 1199 FPETDKWIEIGETEGKFIVDSVELLMEE 1228

Db 1198 FPETDKWIEIGETEGKFIVDSVELLMEE 1227

RESULT 6

AAAR50955
ID AAR50955 standard; protein; 1228 AA.

AAAR50955;

AC

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 18-OCT-1994 (first entry)

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Bacillus thuringiensis CryIB insecticidal protoxin.
Insecticidal crystal protein; ICP; cryIB; Ostrinea nubilalis;
European corn borer; Lepidoptera; Pyralidae; toxin.
Bacillus thuringiensis; (strain entomocidus HD 110).

EP589110-A1.

30-MAR-1994.

19-AUG-1992; 92EP-00402307.

19-AUG-1992; 92EP-00402307.

(PLBZ) PLANT GENETIC SYSTEMS NV.

Peferoen M, Jansens S, Denolf P;

WPI; 1994-102862/13.

N-PSDB; AAQ56804.

Method to control or combat Ostrinia - utilises Bacillus thuringiensis
cry IB gene/protein for crop prevention.

Claim 1; Page 11-18; 38pp; English.

The CryIB toxin gene (disclosed in EP-408403) has been found to be toxic
to the European corn borer (Ostrinea nubilalis). The use of CryIB
insecticidal crystal protein for protecting crops against O.nubilalis is
claimed. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT
-2003 to standardise OS field)

Sequence 1228 AA;

Query Match 88.6%; Score 5740; DB 2; Length 1228;
Best Local Similarity 89.0%; Pred. No. 0;

Matches 1097; Conservative 36; Mismatches 90; Indels 10; Gaps 3;

QY 1 LTSNRKNEIINALSTIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVOTGI 60

Db 1 MTSNRKNEIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVOTGI 55

QY 61 NIAGRIILGVLPVPPAGQIASFYSPFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 120

Db 56 NIAGRIILGVLPVPPAGQIASFYSPFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTA 115

QY 121 LARLQGLGDSFRAYQQSLEDWLENRRDARTSRVLYTQYIALELDPLNAMPLFAIRNQVVP 180

Db 116 LARLQGLGDSFRAYQQSLEDWLENRRDARTSRVLYTQYIALELDPLNAMPLFAIRNQVVP 175

QY 181 LLMVYAQAANLHLLLRDLASLFGSEFGLTSQEIQRYYERQVQEQTRDYSYCVVWYNTGLN 240

Db 176 LLMVYAQAANLHLLLRDLASLFGSEFGLTSQEIQRYYERQVQEQTRDYSYCVVWYNTGLN 235

QY 241 SLRGTTNAASWVRNQFRDLITGLVDLVALFSPYDTRTPINTSAQLTREYVTDIGRTN 300

Db 236 SLRGTTNAASWVRNQFRDLITGLVDLVALFSPYDTRTPINTSAQLTREYVTDIGRTN 295

QY	301	VNMASWYNNAPSAFSAETAVIETSPHLLDFLEQLTIFSTSSRWASATRHMTYWRGHTIQ	360
Db	296	VNMASWYNNAPSAFSAETAVIETSPHLLDFLEQLTIFSTSSRWASATRHMTYWRGHTIQ	355
QY	361	SRPIGGGLNTSTHGSTNTSINPVLRSFPFSRDVYWTESYAGVLLMGILYLEPIHGVPTVRFN	420
Db	356	SRPIGGGLNTSTHGATNTSINPVTLPFASRDVYRTESYAGVLLMGILYLEPIHGVPTVRFN	415
QY	421	FRNPQNTPERGTANYSQPYESGLQKDSLETLPETTERPNYESYSHRLSHIGLISQSR	480
Db	416	FTNPQNISDRGTANYSQPYESGLQKDSLETLPETTERPNYESYSHRLSHIGLISQSR	475
QY	481	VAVPVYSWTHRSADRTNTISSDIITQIPLVKSFXNLNSGTSVVSGPFTGGDIIRTNVNGS	540
Db	476	VNPVYSWTHRSADRTNTIGPNRITQIPMVKASELPQGTITVVRGPGFTGGDILARTTGG	535
QY	541	VLSMGLNFANTSLQRYRVYRVAASQTVLVRVYVGGSTTFDQGPSPMTSANESLTSOSFR	600
Db	536	FGPIRVTVNGPLTQRYRGFRYASIVDFFVSRGGITVNNFRFLRTNWSGDELYKGNFV	595
QY	601	FAEPFVGISASGQ-TAGISISNNAGRQTHFDKIEFIPITATPEAEYDLERAQEAVAL	659
Db	596	RRAPTPPTFTQIODIIRTSIQGLSGNCEVVIDKIEIIPVPTATPEAEYDLERAQEAVAL	655
QY	660	FNTNTPRLKTDVTDYHIDOVSNLVACLSDSEFCIDKREKLEKVKYAKRLSDERNLLQDP	719
Db	656	FNTNTPRLKTDVTDYHIDOVSNLVACLSDSEFCIDKREKLEKVKYAKRLSDERNLLQDP	715
QY	720	NFTSNKQPDFISTNEQSNFTSIHQSBHGMWGSNTIIOEGNDVPKENVYVTLPGTFNEC	779
Db	716	NFTSNKQPDFISTNEQSNFTSIHQSBHGMWGSNTIIOEGNDVPKENVYVTLPGTFNEC	775
QY	780	YPTLYYQKIGSELKAXTRYQLRGVIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVE	839
Db	776	YPTLYYQKIGSELKAXTRYQLRGVIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVE	835
QY	840	SPIGRCGPNRCAPHEFWNPDLDCSCRCRGEKCAHSHHFSLDIIDIGCTDLHENLGWVWF	899
Db	836	SPIGRCGPNRCAPHEFWNPDLDCSCRCRGEKCAHSHHFSLDIIDIGCTDLHENLGWVWF	895
QY	900	KIKTOEGHARLGNLEFIEEKLPLGBALSRVRAEKKWRDKREKLOLETKRVTYEAKEAVD	959
Db	896	KIKTOEGHARLGNLEFIEEKLPLGBALSRVRAEKKWRDKREKLOLETKRVTYEAKEAVD	955
QY	960	ALFVDSQYNRLQADTNIGMIIHAADKLVHRIEAYLSLSEVIPGVNABIFEELEGRIITAI	1019
Db	956	ALFVDSQYDRLQADTNIGMIIHAADKLVHRIEAYLSLSEVIPGVNABIFEELEGRIITAI	1015
QY	1020	SLYDARNVYKGGDFNGLACMNVKGVHDVQOSHRSVLVLPWEAEVYSQAVRVCPRGYI	1079
Db	1016	SLYDARNVYKGGDFNGLTCWNVKGHVHDVQOSHRSOLVLPWEAEVYSQAVRVCPRGYI	1075
QY	1080	LRVTAKEGKGEGCVTIIHEIENNTDELKFKNCEEEVYPTDTGTCDNYTAHQGTA---V	1135
Db	1076	LRVTAKEGKGEGCVTIIHEIENNTDELKFKNCEEEVYPTDTGTCDNYTAHQGTAGCADA	1135
QY	1136	CNSRNAGYEDAYEVDTTASVNYKPYEETTYDVRDNNHCEYDRGYVNYPLPAGYMTKE	1195
Db	1136	CNSRNAGYEDAYEVDTTASVNYKPYEETTYDVRDNNHCEYDRGYVNYPPVAGYVTKK	1195
QY	1196	LEYFPETDKWIEIGETGKFIIVDSVELLLMEE	1228
Db	1196	LEYFPETDKWIEIGETGKFIIVDSVELLLMEE	1228

RESULT 7
AAY31990
ID AAY31990 standard; protein; 1227 AA.

DE	Chimeric Cry1B insecticide HyFL1B.
XX	Insecticide; HyFL1B; crystal protein; delta-endotoxin; toxin; cry1B;
KW	Cry1A(b); maize; transgenic plant; European corn borer;
KW	Ostrinia nubilalis; entomocide; crop protection; biological control.
XX	
OS	Bacillus thuringiensis.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Protein 1..845
FT	note= "cry1B"
FT	Protein 846..1227
FT	/note= "cry1A(b)"
XX	
XX	W09950293-A1.
PN	
XX	
XX	07-OCT-1999.
PD	
XX	
XX	30-MAR-1999; 99WO-EF002175.
PF	
XX	
XX	01-APR-1998; 98US-00053549.
PR	
XX	
XX	(NOVS) NOVARTIS AG.
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PI	
XX	Desai NM;
XX	
XX	WPI; 1999-601323/51.
DR	N-PSDB; AAZ20086.
DR	
XX	
XX	Chimeric insecticidal protein comprising cry1B and cry1A(b) portions.
PT	
XX	
XX	Claim 12; Page 43-47; 85pp; English.
PS	
XX	
XX	This sequence represents a chimeric insecticidal protein, termed hyFL1B,
CC	that is composed of a cry1B core N-terminal toxin portion of 845 amino
CC	acids and a cry1A(b) C-terminal protoxin portion of 382 amino acids. The
CC	cry1B and cry1A(b) portions of the synthetic gene (see AAZ20086) encoding
CC	hyFL1B were derived from Bacillus thuringiensis with codon usage altered
CC	to increase expression in plants, particularly maize. When the chimeric
CC	insecticidal protein gene is expressed in transgenic maize from both pEPc
CC	and pith promoters, insecticidal activity is observed against European
CC	corn borer (Ostrinia nubilalis). Recombinant microbial strains
CC	transformed with the hyFL1B gene can be used in endotomocidal formulations
CC	for the biological control of Lepidopteran pests
XX	
SQ	Sequence 1227 AA;

Qy	181	LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEGTRDYSDYCVWYNTGLN	240
Db	176	LLMVYAQAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVEGTRDYSDYCVWYNTGLN	235
Qy	241	SLRGTTNAASWVRYNQFRDLTLGLVLALFPSYDTRTYPINTSAOLTREVVYDAIGATG	300
Db	236	SLRGTTNAASWVRYNQFRDLTLGLVLALFPSYDTRTYPINTSAOLTREVVYDAIGATG	295

Db 479 GNTLRAPVSWTHRSADRTNTIGPNRITQIPLVKALNLSHGVTVGGPGFTGGDILRRTN 538
 Qy 538 NGSVLSMGLNFNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTFDQGPSTMTSANEISLTSQ 597
 Db 539 TGTGDIRLNLINPLSQRVRVIRYASTTDLQFFTRINGTTVNIQNFSTRMGRGNLEVR 598
 Qy 598 SRPRAPFPVIGISASGQTAGISISNAGRQTFHFKIEFIPITATFEAYDYLERAEAVN 657
 Db 599 SFRTAGFSTFPFLNAQSTFTLGAQSFSNQEVYDRVEFVPAEVTFEAYDYLERAKAVN 658
 Qy 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSEFCLDEKRELEKVKYAKRLSDERNLQ 717
 Db 659 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSEFCLDEKRELEKVKYAKRLSDERNLQ 718
 Qy 718 DNFNFTSINKQDPFISTNEQSNFTSIHQSEHGWSGSENITIQEGNDVFKENVYTLPGTFN 777
 Db 719 DNFNFTISQLSFASIDGQSNFPISELSEHGWSGANVTIQEGNDVFKENVYTLPGTFN 778
 Qy 778 ECPYTYLYOKIGESLKVATRYQLRGYIEDSODLEIYLIRYNAKHETLDVPGTESWPLS 837
 Db 779 ECPYNYLYKIGESLKVATRYQLRGYIEDSODLEIYLIRYNAKHETLDVPGTSLWPLS 838
 Qy 838 VESPIGRCEPNRCAPHPFNWPDLCSCRDGKCAHSHHPSLDDIGCTDLHENLGVWV 897
 Db 839 VESPIGRCEPNRCAPHPFNWPDLCSCRDGKCAHSHHPSLDDIGCTDLHENLGVWV 898
 Qy 898 VFPIKTOEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLOLETKEVYTEAKEA 957
 Db 899 VFPIKTOEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLOLETKEVYTEAKEA 958
 Qy 958 VDALLFVDSQYNRLQADTNIGMTHAADKLVHRIEAYLSLSVIGPVNAEIPBELEGRIIT 1017
 Db 959 VDALLFVDSQYNRLQADTNIGMTHAADKLVHRIEAYLSLSVIGPVNAEIPBELEGRIIT 1018
 Qy 1018 ALSYDARVNGKPNGLACWNVKGVVDVQOSSHRSVLVYIPEHEAEVSQAVRVCGRG 1077
 Db 1019 AMSLYDARVNGKPNGLACWNVKGVVDVQOSSHRSVLVYIPEHEAEVSQAVRVCGRG 1078
 Qy 1078 YILRTAYKEGEGECVTHETENNTDELKFNCEBEVYPTDTGTCNDYTAHQGTAVCN 1137
 Db 1079 YILRTAYKEGEGECVTHETENNTDELKFNCEBEVYPTDTGTCNDYTAHQGTAVCN 1138
 Qy 1138 SRNAGYEDAYEDVTTASVNYKPYEETVTVRRDNHCEYDRGYVNYPLPAGYMTKLE 1197
 Db 1139 SRNAGYEDAYEDVTTASVNYKPYEETVTVRRDNHCEYDRGYVNYPPVAGYVTKLE 1198
 Qy 1198 YPPEYDKWIEIGETEGKFIUDSVELLME 1228
 Db 1199 YPPEYDKWIEIGETEGKFIUDSVELLME 1229

RESULT 9

AAW35259
 ID AAW35259 standard; protein; 1229 AA.

AC AAW35259;

XX 17-FEB-1998 (first entry)

XX Bacillus thuringiensis crystal toxin Cry5T5.

DE EG7283; crystal toxin; Cry5T5; lepidopteran pest; *Lymantria dispar*;
 KW *Ostrinia nubilalis*; *Pseudoplusia includens*; *Plutella xylostella*;
 KW *Spodoptera exigua*; *Spodoptera frugiperda*; *Trichoplusia ni*.

XX Bacillus thuringiensis.

OS US5679343-A.

PN 21-OCT-1997.

PD 07-JUN-1995; 95US-00474038.

XX

PR 29-JUL-1993; 93US-00100709.
 PR 30-DEC-1993; 93US-00176865.
 XX (MONS) MONSANTO CO.
 PI Jany CS, Gonzalez JM, Donovan WP, Tan Y;
 DR WPI; 1997-525682/48.
 DR N-PSDB; AAT95051.
 XX Lepidopteran toxic Bacillus thuringiensis crystal protein - useful to
 PT control Lepidopteran pests.
 PS Claim 2; Fig 2; 50pp; English.
 XX The present sequence is the Bacillus thuringiensis EG7283 crystal toxin
 CC Cry5T5, which, optionally in association with B. thuringiensis EG7283,
 CC can be used against lepidopteran pests. Cry5T5 is especially useful for
 CC controlling *Lymantria dispar*, *Ostrinia nubilalis*, *Pseudoplusia includens*,
 CC *Plutella xylostella*, *Spodoptera exigua*, *Spodoptera frugiperda* and
 CC *Trichoplusia ni*
 XX Sequence 1229 AA;

Query Match 80.8%; Score 5237.5; DB 2; Length 1229;
 Beat Local Similarity 79.9%; Pred. No. 0;
 Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;
 Qy 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEAGNNINPLVSASTVQTGI 60
 Db 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEAGNNINPLVSASTVQTGI 60
 Qy 61 NIAGRIILGVLPAGQIASFVSLVGLWELPRGDOWEIFLEHVQLINQOITENARNTA 120
 Db 61 NIAGRIILGVLPAGQIASFVSLVGLWELPRGDOWEIFLEHVQLINQOITENARNTA 120
 Qy 121 LARLQGLGDSFRAYQQSLIEDMLNRRDARTASVLTQYIALELDFLNAMPLFAIRNOEVP 180
 Db 121 LARLQGLGDSFRAYQQSLIEDMLNRRDARTASVLTQYIALELDFLNAMPLFAIRNOEVP 180
 Qy 181 LLMVYAQANLHLLLRDASLFGSEFGLTSQEIQRVYERQVEQTRDYSDYCVIEWNTGLN 240
 Db 181 LLMVYAQANLHLLLRDASLFGSEFGLTSQEIQRVYERQVEQTRDYSDYCVIEWNTGLN 240
 Qy 241 SLRGTAASVRYNQFREDLTLGVLDLVALPSPYDTRTPYNTSAQLTRVYVTDAGTGTG 300
 Db 241 SLRGTAASVRYNQFREDLTLGVLDLVALPSPYDTRTPYNTSAQLTRVYVTDAGTGTG 300
 Qy 301 V--NMASMNWNNNAPSPSAIETAVIRSPHLLDLEQLTIFSTSRMSATRHMTYWRGHT 358
 Db 301 V--NMASMNWNNNAPSPSAIETAVIRSPHLLDLEQLTIFSTSRMSATRHMTYWRGHT 358
 Qy 359 IQSRPIGGLNTSTHGST-NTSINPVRSLSPSRDVYMTESVAGVLLWGIYLEPIHGVPV 417
 Db 359 IQSRPIGGLNTSTHGST-NTSINPVRSLSPSRDVYMTESVAGVLLWGIYLEPIHGVPV 417
 Qy 418 RFNFRNPQNTPERGTANYSPQSPGLQKDSFELPPEPPERPERNYESYHRLSHIGLIS 477
 Db 418 RFNFRNPQNTPERGTANYSPQSPGLQKDSFELPPEPPERPERNYESYHRLSHIGLIS 477
 Qy 478 QSRVHVVPYSWTHRSADRTNTISSDSITQIPLVKSNLNSGTSVVSGPGFTGGDIIRTNV 537
 Db 478 QSRVHVVPYSWTHRSADRTNTISSDSITQIPLVKSNLNSGTSVVSGPGFTGGDIIRTNV 537
 Qy 479 GNTLRAPVSWTHRSADRTNTIGPNRITQIPLVKALNLSHGVTVGGPGFTGGDILRRTN 538
 Db 479 GNTLRAPVSWTHRSADRTNTIGPNRITQIPLVKALNLSHGVTVGGPGFTGGDILRRTN 538
 Qy 538 NGSVLSMGLNFNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTFDQGPSTMTSANEISLTSQ 597
 Db 538 NGSVLSMGLNFNTSLQRYRVRVRYAASQTMVLRTVTVGGSTTFDQGPSTMTSANEISLTSQ 597
 Qy 598 SFRAPFPVIGISASGQTAGISISNAGRQTFHFKIEFIPITATFEAYDYLERAEAVN 657
 Db 598 SFRAPFPVIGISASGQTAGISISNAGRQTFHFKIEFIPITATFEAYDYLERAEAVN 657
 Qy 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSEFCLDEKRELEKVKYAKRLSDERNLQ 717
 Db 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSEFCLDEKRELEKVKYAKRLSDERNLQ 717

[illegible]

RESULT 11

AAW87633	standard; protein; 1229 AA.
AAW87633	
AAW87633	
03-MAR-1999	(first entry)
CryET5	protein sequence.
CryET4	Bacillus thuringiensis strain EG5847; crystal toxin; CryET5;
Lepidoptera	Helicoverpa zea; resistant strain; Plutella xylostella;
Spodoptera	exigua; S. frugiperda; S. frugiperda; Trichoplusia ni.
Bacillus	thuringiensis.
US5854053-A.	
29-DEC-1998.	
06-JAN-1997;	97US-00779046.
29-JUL-1993;	93US-00100709.
30-DEC-1993;	93US-00176865.
07-JUN-1995;	95US-00474038.
ECOG--	ECOGEN INC.
Donovan WP,	Gonzalez JM;
WPI;	1999-094915/08.
N-PSDB;	AAV83927.
New strains	EG5847 and EG10368 of Bacillus thuringiensis - producing
crystal	toxins active against Lepidoptera, particularly Helicoverpa zea,
Plutella	xylostella and spodoptera species.

QY 838 VESPIGRCEPNRCAPHFENWPDLCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVWV 897
 Db 839 VESPIGRCEPNRCAPHFENWPDLCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVWV 898
 QY 898 VFQIKTQEGHARLGNLEFIEEKPLLEALSRVKAERKWRDKREKQLQLETKRVYTEAKEA 957
 Db 899 VFQIKTQEGHARLGNLEFIEEKPLLEALSRVKAERKWRDKREKQLQLETKRVYTEAKEA 958
 QY 958 VDAPLVDSQYNRLQADNTNIGMTHAADKLVHRIEAYLSLSVPGVNAEIEFELEGRIIT 1017
 Db 959 VDAPLVDSQYNRLQADNTNIGMTHAADKLVHRIEAYLSLSVPGVNAEIEFELEGRIIT 1018
 QY 1018 AISLYDARNVKNQGFNNGLACWNVKGVQVQSHRSVLVTPWEAEVSAQVRVCPGRG 1077
 Db 1019 ANSLYDARNVKNQGFNNGLTCWNVKGVQVQSHRSVLVTPWEAEVSAQVRVCPGRG 1078
 QY 1078 YILRVYAYKEGEGECVTIHEIENNTDELKFNCEEEVYPTDTGTCNDYTAHQGTACVN 1137
 Db 1079 YILRVYAYKEGEGECVTIHEIENNTDELKFNCEEEVYPTDTGTCNDYTAHQGTACVN 1138
 QY 1138 SRNAGVEDAYEDVTTASVNYKPYEETTYTDRRDNHCEYDGVNYPPLPAGVYTKELE 1197
 Db 1139 SRNAGVEDAYEDVTTASVNYKPYEETTYTDRRDNHCEYDGVNYPPLPAGVYTKELE 1198
 QY 1198 YPPTDKVWIEIGETEGKFIIVDSVELLMEE 1228
 Db 1199 YPPTDKVWIEIGETEGKFIIVDSVELLMEE 1229

RESULT 12

AAV30923

ID AAV30923 standard; protein; 1229 AA.

XX AC AAV30923;

DT 18-OCT-1999 (first entry)

XX DE B. thuringiensis cryET5 partial protein.

XX KW Toxin; cryET4; cryET5; insecticidal; Lepidoptera; transformed plant;

XX OS Bacillus thuringiensis.

XX FH Key

XX FT Protein

XX FT 1. 1229

XX FT /note= "partial protein sequence. No ATG start codon

XX FT given"

XX PN US5942658-A.

XX PD 24-AUG-1999.

XX PF 24-JUN-1997; 97US-00881340.

XX PR 29-JUL-1993; 93US-00100709.

XX PR 30-DEC-1993; 93US-00176865.

XX PR 07-JUN-1995; 95US-00474038.

XX PA (MONS) MONSANTO CO.

XX XX Gonzalez JM, Jany CS, Tan Y, Donovan WP;

XX XX WPI; 1999-493544/41.

XX XX N-PSDB; AA209160.

XX PT Transformed plant comprising insecticidal crystal proteins.

XX PS Claim 3; Fig 2A-J; 50pp; English.

XX CC This invention describes novel transformed plants containing Bacillus

XX CC thuringiensis strain EG5847 insecticidal crystal protein genes cryET4 or

XX CC cryET5. cryET4 and cryET5 are novel toxin genes which produce

CC insecticidal proteins with activity against a broad spectrum of insects
 CC of the order Lepidoptera. This sequence represents the cryET5 protein
 CC described in the method of the invention

XX SQ Sequence 1229 AA;

Query Match 80.8%; Score 5237.5; DB 2; Length 1229;
 Best Local Similarity 79.9%; Pred. No 0;
 Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

QY 1 LTSNRKNEIINALSIPAVSNHSTQWLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60

Db 1 LTSNRKNEIINALSIPAVSNHSTQWLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60

QY 61 NIAGRILGVLPFAGQIASFYSLGELWPGRDQWEIPLHVEQLINQQTENARNTA 120

Db 61 NIAGRILGVLPFAGQIASFYSLGELWPGRDQWEIPLHVEQLINQQTENARNTA 120

QY 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSVLYTYQYIALELDLFNAMPLFAIRNOEVP 180

Db 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSVLYTYQYIALELDLFNAMPLFAIRNOEVP 180

QY 181 LLMVYAQAANLHLLLRDASLFGSFGSLTSQBIQRYERQVQTRDYSYCVENYNTGN 240

Db 181 LLMVYAQAANLHLLLRDASLFGSFGSLTSQBIQRYERQVQTRDYSYCVENYNTGN 240

QY 241 SLRGTNAAWVRVYNQFRDLTLGLVLDLVALPSPYDTRTYPINTSAQLTREYTDIGATG 300

Db 241 SLRGTNAAWVRVYNQFRDLTLGLVLDLVALPSPYDTRTYPINTSAQLTREYTDIGATG 300

QY 301 V-NNASMMWYNNAPSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATHMTYWRGT 358

Db 301 V-NNASMMWYNNAPSAIETAVIRSPHLLDFLEQLTIFSTSSRWASATHMTYWRGT 358

QY 359 IQSRPIGGGLNTSTHGST-NTSINPVLSFSDRVVWTSYAGVLLWGIYIPIHGVTPT 417

Db 359 IQSRPIGGGLNTSTHGST-NTSINPVLSFSDRVVWTSYAGVLLWGIYIPIHGVTPT 417

QY 418 RNFNPQNTFERGTANYSPQYSPGLQKDSLETLPETTERPNYESYSHRLSHIGLIS 477

Db 418 RNFNPQNTFERGTANYSPQYSPGLQKDSLETLPETTERPNYESYSHRLSHIGLIS 477

QY 478 QSRVHPVYVWTHRSADRTNTISSDITQIPLVSKFNLNSGTSVVGSGFTGGDIIRNV 537

Db 478 QSRVHPVYVWTHRSADRTNTISSDITQIPLVSKFNLNSGTSVVGSGFTGGDIIRNV 537

QY 538 NGSVLSMGLNFNTSLQRYVRVRYAASQTMVLRVTVGSGTTFDQGFSTWSANESLTSQ 597

Db 538 NGSVLSMGLNFNTSLQRYVRVRYAASQTMVLRVTVGSGTTFDQGFSTWSANESLTSQ 597

QY 598 SFRFAEPVGISASGSGTAGISINNAGRQTFHFKIEFIPITATFBAEYDLERAQAVN 657

Db 598 SFRFAEPVGISASGSGTAGISINNAGRQTFHFKIEFIPITATFBAEYDLERAQAVN 657

QY 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLKVKYAKLSERNLLO 717

Db 658 ALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLKVKYAKLSERNLLO 717

QY 718 DPNFTSINKQDPFITSTNEQNFSTSIHQSEHGMWSENITIQEGNVFKENYVTLPGTFN 777

Db 718 DPNFTSINKQDPFITSTNEQNFSTSIHQSEHGMWSENITIQEGNVFKENYVTLPGTFN 777

QY 778 ECPYLYQKIGESELKAYTRYQLRGYIEDSQDLIELYLRYNKHEHLDVPGTESVWPLS 837

Db 778 ECPYLYQKIGESELKAYTRYQLRGYIEDSQDLIELYLRYNKHEHLDVPGTESVWPLS 837

QY 838 VESPIGRCEPNRCAPHFENWPDLCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVWV 897

Db 838 VESPIGRCEPNRCAPHFENWPDLCSCRDGKCAHSHHFLSDIDIGCTDLHENLGVWV 897

QY 898 VFQIKTQEGHARLGNLEFIEEKPLLEALSRVKAERKWRDKREKQLQLETKRVYTEAKEA 957

Db 898 VFQIKTQEGHARLGNLEFIEEKPLLEALSRVKAERKWRDKREKQLQLETKRVYTEAKEA 957

QY 958 VDALFVDSQYNRLQADTNIGMIHAADKLVHRIEAYLSLSVPGVNAEIFEELGRIT 1017
 DB 959 VDALFVDSQYDQADTNIGMIHAADKLVHRIEAYLSLSPVPGVNAEIFEELGHIIT 1018
 QY 1018 AISLYDARNVKNNGDNGLACWNVKGVHDVQOSHRSVLVTPWEAEVSAQVRVCPGRG 1077
 DB 1019 AMSLYDARNVKNNGDNGLTCWNVKGVHDVQOSHRSVLVTPWEAEVSAQVRVCPGRG 1078
 QY 1078 YILRTVAYKEGEGCVTTHETNNDELKFNCEEEVYPTDGTCDNDYTAHQGTAVCN 1137
 DB 1079 YILRTVAYKEGEGCVTTHETNNDELKFNCEEEVYPTDGTCDNDYTAHQGTAVCN 1138
 QY 1138 SRNAGYDAYEYDVTASVNYKPYEETVTVRRDNHCEYDRGYVNYPLPAGYMTKELE 1197
 DB 1139 SRNAGYDAYEYDVTASVNYKPYEETVTVRRDNHCEYDRGYVNYPPVPGYVTKLE 1198
 QY 1198 YPPTDKWIEIGETEGKFIIVDSVELLMEE 1228
 DB 1199 YPPTDKWIEIGETEGKFIIVDSVELLMEE 1229

RESULT 13

ADK98479

ID ADK98479 standard; protein; 1229 AA.

AC ADK98479;

XX 03-JUN-2004 (first entry)

XX B thuringiensis cry1Bb partial protein sequence SeqID2.
 DE insecticidal protein; plant; pesticide; gene therapy;
 KW lepidopteran insect pest; transgenic plant;
 KW insect infestation resistance; monocot; dicot; cry1Bb.

XX Bacillus thuringiensis.

XX WO2004020636-A1.

XX 11-MAR-2004.

XX 26-AUG-2003; 2003WO-US026510.

XX 29-AUG-2002; 2002US-0407428P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX (BOGD/) BOGDANOVA N N.

XX (ROMA/) ROMANO C P.

XX Bogdanova NN, Romano CP;

XX WPI; 2004-269221/25.

XX DR N-P5DB; ADK98478.

XX New polynucleotide sequence optimized for expression of an insecticidal
 PT protein in a plant, useful in the control of Lepidoptera insect pests,
 PT and for producing transgenic plants with the ability to resist insect
 PT infestations.

XX Claim 7; SEQ ID NO 2; 138pp; English.

XX This invention relates to a novel polynucleotide sequence optimised for
 CC expression of an insecticidal protein in a plant. The invention may be
 CC useful for the production of pesticides whilst the disclosed sequences
 CC may be used for gene therapy. The polynucleotide sequence and methods are
 CC useful in the control of lepidopteran insect pests, and for producing
 CC transgenic plants with the ability to resist insect infestations. The
 CC invention provides polynucleotide sequences with enhanced, improved and
 CC optimised expression in monocot and dicot plant species. The present
 CC sequence is that of the (partial) B thuringiensis cry1Bb protein which is
 CC related to the invention.

SQ Sequence 1229 AA;

Query Match 80.8%; Score 5237.5; DB 8; Length 1229;

Best Local Similarity 79.9%; Pred. No. 0;

Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSDPARIEDSLCIAEGNNINPLVSASTVQTGI 60
 DB 1 LTSNRKNEIINALSIPAVSNHSTQMDLSDPARIEDSLCIAEGNNINPLVSASTVQTGI 60
 QY 61 NIAGRIILGVLPAGQIATSFYFLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
 DB 61 NIAGRIILGVLPAGQIATSFYFLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
 QY 121 LARLQGLGDSFRAVQOQSLDMLNRRDARTSVLTVQVIALELDPLNAMPLPAIRNQVVP 180
 DB 121 LARLQGLGDSFRAVQOQSLDMLNRRDARTSVLTVQVIALELDPLNAMPLPAIRNQVVP 180
 QY 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSGEIQRYRYERQVEQTRDYSDYCVWEVNTGLN 240
 DB 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSGEIQRYRYERQVEQTRDYSDYCVWEVNTGLN 240
 QY 241 SLRGTTAAASVRYNQFRDLTLGLVLDLVALPSPVDTTRYPIINTSAQLTREVYTDAGTG 300
 DB 241 NLRGTTAAASVRYNQFRDLTLGLVLDLVALPSPVDTTRYPIINTSAQLTREVYTDAGTG 300
 QY 301 V--NWASMNWYNNNAPSPSAIETAVIRSPHLLDLEQLTIFSTSRWSATRHMTYRGHT 358
 DB 301 APSGFASNTWNNNAPSPSAIETAVIRSPHLLDLEQLTIFSTSRWSATRHMTYRGHT 358
 QY 359 IQSRPIGGGLNTSTHGST--NTSINPVRLSFSDVYMTESYAGVLLWGLYIEPIHGVPV 417
 DB 359 IQSRPIGGGLNTSTHGST--NTSINPVRLSFSDVYMTESYAGVLLWGLYIEPIHGVPV 417
 QY 361 LNFRIPIGGLNTSTHGST--NTSINPVRLSFSDVYMTESYAGVLLWGLYIEPIHGVPV 418
 DB 361 LNFRIPIGGLNTSTHGST--NTSINPVRLSFSDVYMTESYAGVLLWGLYIEPIHGVPV 418
 QY 418 RNFNRPNPTPRTGTYANYSQPYEGLQKQDSELTPELTPETTERPNYRYSRHLSHIGLIS 477
 DB 418 RNFNRPNPTPRTGTYANYSQPYEGLQKQDSELTPELTPETTERPNYRYSRHLSHIGLIS 477
 QY 478 QSRVHVVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTVSVSGPGFTGGDIIRNV 537
 DB 478 QSRVHVVPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTVSVSGPGFTGGDIIRNV 537
 QY 479 GNTLRAPVYVSWTHRSADRTNTIGPNRITQIPLVKSFNLSGTVSVSGPGFTGGDIIRNV 538
 DB 479 GNTLRAPVYVSWTHRSADRTNTIGPNRITQIPLVKSFNLSGTVSVSGPGFTGGDIIRNV 538
 QY 538 NGSVLSMGLNNTSLQRYRVRYAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQ 597
 DB 538 NGSVLSMGLNNTSLQRYRVRYAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQ 597
 QY 539 TGTFGDIRLNLNINPLSQRYRVRYAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQ 598
 DB 539 TGTFGDIRLNLNINPLSQRYRVRYAASQTMVLRTVTVGGSTTFDQGPSTMSANESLTSQ 598
 QY 598 SFRFAEPFVGISASGQTAGISISNNAGRTFFHFKIEFIPITATFEAYDLERAQEA 657
 DB 598 SFRFAEPFVGISASGQTAGISISNNAGRTFFHFKIEFIPITATFEAYDLERAQEA 657
 QY 599 SFRFAEPFVGISASGQTAGISISNNAGRTFFHFKIEFIPITATFEAYDLERAQEA 658
 DB 599 SFRFAEPFVGISASGQTAGISISNNAGRTFFHFKIEFIPITATFEAYDLERAQEA 658
 QY 658 ALFTNTNPRRLKTDVTHIDVSNLVACLSDEECLOEKRELLKVKYAKLSDERNLQ 717
 DB 658 ALFTNTNPRRLKTDVTHIDVSNLVACLSDEECLOEKRELLKVKYAKLSDERNLQ 717
 QY 718 ALFTNTNPRRLKTDVTHIDVSNLVACLSDEECLOEKRELLKVKYAKLSDERNLQ 718
 DB 718 ALFTNTNPRRLKTDVTHIDVSNLVACLSDEECLOEKRELLKVKYAKLSDERNLQ 718
 QY 718 DPNTFTSINKQPDFISTNEQSNFTSIHSESHGWSGNSITIQEGNDVFKENYVTLPGTFN 777
 DB 718 DPNTFTSINKQPDFISTNEQSNFTSIHSESHGWSGNSITIQEGNDVFKENYVTLPGTFN 777
 QY 719 DPNTFTSINKQPDFISTNEQSNFTSIHSESHGWSGNSITIQEGNDVFKENYVTLPGTFN 778
 DB 719 DPNTFTSINKQPDFISTNEQSNFTSIHSESHGWSGNSITIQEGNDVFKENYVTLPGTFN 778
 QY 778 ECPYTYLYQKIGSELSKAYTRYQLRGVYEDSQDLLEIYLIRYNAKHETLDVPGTSVWPLS 837
 DB 778 ECPYTYLYQKIGSELSKAYTRYQLRGVYEDSQDLLEIYLIRYNAKHETLDVPGTSVWPLS 837
 QY 838 VESPIGRCGEPRNRCAPHFENWPDLDCCRCDEKCAHSHHSHSLDIDGCTDLHENLGVW 897
 DB 838 VESPIGRCGEPRNRCAPHFENWPDLDCCRCDEKCAHSHHSHSLDIDGCTDLHENLGVW 897
 QY 898 VFKIKTOEGHARLGNLNFIEBKPLLGALSRSVKAEEKWRDKREKQLQETKRVYTEAKEA 957
 DB 898 VFKIKTOEGHARLGNLNFIEBKPLLGALSRSVKAEEKWRDKREKQLQETKRVYTEAKEA 957
 QY 958 VDALFVDSQYNRLQADTNIGMIHAADKLVHRIEAYLSLSVPGVNAEIFEELGRIT 1017
 DB 958 VDALFVDSQYNRLQADTNIGMIHAADKLVHRIEAYLSLSVPGVNAEIFEELGRIT 1017

Db 1021 MSLEYDARNVKKNGDFNNGITCNWVKGHVDVQOQSHRSDLVLPWEAEVSAQVRVCPGRGY 1080
 QY 1079 ILRVAYKEGYGEGCVTHIEINNTDELKFKNCBEEVYPTDTGTCNDYTAHQGTAVCNS 1138
 Db 1081 ILRVAYKEGYGEGCVTHIEINNTDELKFKNCBEEVYPTDTGTCNDYTAHQGTAAACS 1140
 QY 1139 RNAGVEDAYEVDTTASVNYKPYEBETVYDVRDNHCEYDRGVVNPPLPAGYMTKELEY 1198
 Db 1141 RNAGVEDAYEVDTTASVNYKPYEBETVYDVRDNHCEYDRGVVNPVPVAGYVTKLEY 1200
 QY 1199 PPTDKWLEIGETGKPFVDSVELLMEE 1228
 Db 1201 PPTDTVWLEIGETGKPFVDSVELLMEE 1230

RESULT 15

ADK98489
 ID ADK98489 standard; protein; 1230 AA.

AC ADK98489;

DT 03-JUN-2004 (first entry)

DE B thuringiensis cry1Bb-related expression cassette protein Seq1D12.

XX insecticidal protein; plant; pesticide; gene therapy;
 KW lepidopteran insect pest; transgenic plant;
 KW insect infestation resistance; monocot; dicot; cry1Bb.

XX Bacillus thuringiensis.
 OS Synthetic.

XX WO2004020636-A1.

XX 11-MAR-2004.

XX 26-AUG-2003; 2003WO-US026510.

XX 29-AUG-2002; 2002US-0407428P.

XX (MONS) MONSANTO TECHNOLOGY LLC.
 PA (BOGD/) BOGDANOVA N N.
 PA (ROMA/) ROMANO C P.

XX Bogdanova NN, Romano CP;

XX MPI; 2004-269221/25.

DR N-P5DB; ADK98488.

XX New polynucleotide sequence optimized for expression of an insecticidal
 PT protein in a plant, useful in the control of Lepidoptera insect pests,
 PT and for producing transgenic plants with the ability to resist insect
 PT infestations.

XX Claim 7; SEQ ID NO 12; 138pp; English.

PS This invention relates to a novel polynucleotide sequence optimised for
 CC expression of an insecticidal protein in a plant. The invention may be
 CC useful for the production of pesticides whilst the disclosed sequences
 CC may be used for gene therapy. The polynucleotide sequence and methods are
 CC useful in the control of lepidopteran insect pests, and for producing
 CC transgenic plants with the ability to resist insect infestations. The
 CC invention provides polynucleotide sequences with enhanced, improved and
 CC optimised expression in monocot and dicot plant species. The present
 CC sequence is that of a B thuringiensis cry1Bb expression cassette protein
 CC which is related to the invention.

XX Sequence 1230 AA;

Query Match 80.8%; Score 5233.5; DB 8; Length 1230;
 Best Local Similarity 79.8%; Pred. No. 0;
 Matches 982; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

QY 2 TSNRKNENEIINALSIPAVSNHSTOMDLSDPARIEDSLCAEGNNINPLVSASTVQTGIN 61
 Db 3 TSNRKNENEIINALSIPVSNPSTOMNLSDPARIEDSLCVAEVNIDFVSASTVQTGIN 62
 QY 62 IAGRTLVGLVPPVPAQIASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTAL 121
 Db 63 IAGRTLVGLVPPVPAQIASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQVTTENTRTAI 122
 QY 122 ARLOGLGDSFRAYCOOSLEDWLENDDARTSRVLVYQVYIALELDLFLNAPLFAIRNOEVL 181
 Db 123 ARLEGLGHGYSYQOALETWDNRNDRARSIIILERYVALELDITTAFLFRIRNEEVL 182
 QY 182 LMVYAAQANLHLLLRDASLFGSBSFGLTSQIRYRYERQVEQTRDYSYCVWEYNTGLNS 241
 Db 183 LMVYAAQANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTBYSNHCYQWYNTGLNN 242
 QY 242 LRGTNAASWRYNOFRRLDTLGLVDLVALFPYSYDTRTYPIINTSAQLTREVYDTAIGATGV 301
 Db 243 LRGTNAESWLRYNQFRRLDTLGLVDLVALFPYSYDTRTYPIINTSAQLTREVYDPIGRNA 302
 QY 302 --NMASNNWYNNNAPSASIAETAVRSPLHLDLEOLTIPTSSSEWSATRWYWRGHTI 359
 Db 303 PSGFASTWFWNNAPSASIAEAFRPPHLLDFFPEQLTIYSASSRWSSTOMHNYVWGRHL 362
 QY 360 QSRPIGGGLNTSTHGST-NTSINPVRLSPFSDRVVWTSYAGVLLWGIYLPBPIHGVPVTR 418
 Db 363 NFRPIGGTLNTSTOGLTNTSINPVLTQFTSRDVTYRTSNAGTNI--LFTTPVNGVPPAR 420
 QY 419 FNFRNPQNTFERGTANYSQPYESPOLQKDSLETLPPTTERPNYESYSHRLSHGLISQ 478
 Db 421 FNFINPQNIYERGATTYQPYQGVGIQFDSETLPPTTERPNYESYSHRLSHGLIIG 480
 QY 479 SRVHVYVSWTHRSADRTNTSSDSITQIPLVAKFNLSGTSVYSGRPTGCDIIRTVN 538
 Db 481 NTLRAPVYVSWTHRSADRTNTIGPNRIQIPLVAKNLHSGVTYVGGPGFTGCDILRRNT 540
 QY 539 GSVLSMGLNFNTSLQRYRVRVRAAASQTMVLVTVGGSTTFDQGFPPGTMANESLTSQS 598
 Db 541 GTFGDIRLINVPLSQRYRVRIRYASTDLOFFTRINGTTVNGFNFSYTMARGDNLEYS 600
 QY 599 FRPAEPVGISASGQTAGISISNNAGRQTFPHKIBFIPITATPEABYDLERAQAVNA 658
 Db 601 FRTAGFSTPFNLAQSTFTLGAQSFNSQEVYIDRVBEFVPAEVTPEABYDLERAQAVNA 660
 QY 659 LFTNTPRRLKTDVTDYHIDQVSNLVACLSEFCLEKRELEKVKYAKRLSDERNLQD 718
 Db 661 LFTSTNPRRLKTDVTDYHIDQVSNVACLSEFCLEKRELEKVKYAKRLSDERNLQD 720
 QY 719 PNFTSINKQPDFISTNEQSFTSIHQSEHGWGMSENITIQEGNDVFKENTVTLPGTENE 778
 Db 721 PNFTFISQLSFASIDQSNFSPSINELSEHGWGMSANVTIQEGNDVFKENTVTLPGTENE 780
 QY 779 CYPYLYQKIGESSELKAYTRYQLRGYIEDSDLEIYLIRYNKHEHTLDPGTSVWPLSV 838
 Db 781 CYPNLYQKIGESSELKAYTRYQLRGYIEDSDLEIYLIRYNKHEHTLDPGTSVWPLSV 840
 QY 839 ESPIGRCGEPRNRCAPHFENWPDLDSCRDGKCAHSHHFLSDIDIGCTDLHENLGVWV 898
 Db 841 ESPIGRCGEPRNRCAPHFENWPDLDSCRDGKCAHSHHFLTDIDVGCTDLHENLGVWV 900
 QY 899 FKIKTQSGHARLGNLEFTEEKPLGEALSRVKRAEKWRDKREKLQLETKRYVTEAKAV 958
 Db 901 FKIKTQSGHARLGNLEFTEEKPLGEALSRVKRAEKWRDKREKLQLETKRYVTEAKAV 960
 QY 959 DALFVDSQYNRLQADTNGIMHAADKLVRHIREAYLSLSVPIGVNABIFPELEGRIITA 1018
 Db 961 DALFVDSQYDQADTNGIMHAADKLVRHIREAYLSLSVPIGVNABIFPELEGRIITA 1020
 QY 1019 ISLYDARNVKKNGDFNNGITCNWVKGHVDVQOQSHRSDLVLPWEAEVSAQVRVCPGRGY 1078
 Db 1021 MSLEYDARNVKKNGDFNNGITCNWVKGHVDVQOQSHRSDLVLPWEAEVSAQVRVCPGRGY 1080
 QY 1079 ILRVAYKEGYGEGCVTHIEINNTDELKFKNCBEEVYPTDTGTCNDYTAHQGTAVCNS 1138

Db	1081	ILRVYAYKEGYGECVTHIENNTDELKFNCEEEVYPTDTGTCNDYTAHQGTAA	CNS	1140
Qy	1139	RNAGYEDAYEVDTTASVNYKPTYEEETDVRDNDHCEYDRGVNYPPLPAGYMTKELEY		1198
Db	1141	RNAGYEDAYEVDTTASVNYKPTYEEETDVRDNDHCEYDRGVNYPPVPAGYVYKELEY		1200
Qy	1199	FPETDKWIEIGETEGKFIVDSVELLMEE		1228
Db	1201	FPETDKWIEIGETEGKFIVDSVELLMEE		1230

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Job time : 128 secs

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OM protein - protein search, using sw model

Run on: November 21, 2004, 16:20:51 ; Search time 43 Seconds
(without alignments)
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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5926.5	91.5	1227	1	US-08-448-170-8
3	5926.5	91.5	1227	3	US-08-961-803-9
4	5912.5	91.3	1227	4	US-09-661-322A-63
5	5659.5	87.4	1207	1	US-07-951-715A-7
6	5659.5	87.4	1207	2	US-08-459-448A-7
7	5659.5	87.4	1207	3	US-08-459-595A-7
8	5659.5	87.4	1207	3	US-08-459-504B-7
9	5659.5	87.4	1207	3	US-08-459-444-7
10	5659.5	87.4	1207	3	US-09-053-549-8
11	5659.5	87.4	1207	3	US-09-547-422-7
12	5659.5	87.4	1207	4	US-09-988-462-7
13	5436.5	83.9	1227	3	US-09-053-549-2
14	5237.5	80.8	1229	1	US-08-100-709-4
15	5237.5	80.8	1229	1	US-08-176-865-4
16	5237.5	80.8	1229	2	US-08-474-038-4
17	5237.5	80.8	1229	2	US-08-779-046-4
18	5237.5	80.8	1229	2	US-08-881-340-4
19	5108	78.8	1186	3	US-09-178-252-23
20	5108	78.8	1186	4	US-09-826-660-23
21	3977.5	61.4	1174	1	US-08-040-751-3
22	3977.5	61.4	1174	1	US-08-291-368-2
23	3977.5	61.4	1174	2	US-08-962-190-2
24	3977.5	61.4	1174	5	PCT-US95-10310-2
25	3977.5	61.4	1174	6	5164180-4
26	3791	58.5	1176	1	US-08-434-823-2
27	3791	58.5	1176	1	US-08-457-366-2

28	3579	55.2	1170	1	US-08-032-364-2	Sequence 2, Appli
29	3556	54.9	1167	1	US-08-100-709-2	Sequence 2, Appli
30	3556	54.9	1167	1	US-08-176-865-2	Sequence 2, Appli
31	3556	54.9	1167	1	US-08-474-038-2	Sequence 2, Appli
32	3556	54.9	1167	2	US-08-779-046-2	Sequence 2, Appli
33	3556	54.9	1167	2	US-08-881-340-2	Sequence 2, Appli
34	3502.5	54.1	1189	3	US-09-314-093-59	Sequence 59, Appl
35	3502.5	54.1	1189	3	US-09-314-093-59	Sequence 59, Appl
36	3502.5	54.1	1189	4	US-09-337-635-59	Sequence 59, Appl
37	3502.5	54.1	1189	4	US-09-337-280-59	Sequence 59, Appl
38	3500.5	54.0	1189	2	US-08-980-071-2	Sequence 2, Appli
39	3500.5	54.0	1189	2	US-08-757-536-2	Sequence 2, Appli
40	3500.5	54.0	1189	3	US-09-314-093-2	Sequence 2, Appli
41	3500.5	54.0	1189	3	US-09-250-848-2	Sequence 2, Appli
42	3500.5	54.0	1189	3	US-09-251-885-2	Sequence 2, Appli
43	3500.5	54.0	1189	3	US-09-337-635-2	Sequence 2, Appli
44	3500.5	54.0	1189	4	US-09-337-280-2	Sequence 2, Appli
45	3496.5	54.0	1189	1	US-08-602-737-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-661-322A-38
; Sequence 38, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rel
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661.322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-661-322A-38

Query Match	99.7%	Score 6462;	DB 4;	Length 1228;
Best Local Similarity	99.6%	Pred. No. 0;		
Matches 1223;	Conservative	3;	Mismatches	2; Indels 0; Gaps 0;
Qy	1	LTSNRKNEIINALSIPAVSNHSTQMDLSPDARTEDSLCIAEGNNINPLVSASTVQTGI	60	
Db	1	MTSNRKNEIINALSIPAVSNHSTQMDLSPDARTEDSLCIAEGNNINPLVSASTVQTGI	60	
Qy	61	NIAGRILGLVGPVAGQIASFYSLVGLWELPRGRDQWEIFLEHVQLNQITENARNTA	120	
Db	61	NIAGRILGLVGPVAGQIASFYSLVGLWELPRGRDQWEIFLEHVQLNQITENARNTA	120	
Qy	121	LARIQGLGDSFRAYQQSLEDWLENRRDARTSVLTQVIALELDFLNAMPLFAIRNQVVP	180	
Db	121	LARIQGLGDSFRAYQQSLEDWLENRRDARTSVLTQVIALELDFLNAMPLFAIRNQVVP	180	
Qy	181	LLMVAQAANLHLLLRDASLFGSEFGTISOEIOYRYEROVEOTRDYSDYCVWNTGLN	240	
Db	181	LLMVAQAANLHLLLRDASLFGSEFGTISOEIOYRYEROVEOTRDYSDYCVWNTGLN	240	
Qy	241	SLRGNTAASWRYNQFRDLTLGLVLDLVALPFPSTYDTRTPINTSAQLFREYVYTDAGTG	300	
Db	241	SLRGNTAASWRYNQFRDLTLGLVLDLVALPFPSTYDTRTPINTSAQLFREYVYTDAGTG	300	
Qy	301	VNMASMNWYNNNAPFSFAIETAVIRSPHLLDFLQTLTIFSTSSRWSATRHMTYWRGHTIQ	360	
Db	301	VNMASMNWYNNNAPFSFAIETAVIRSPHLLDFLQTLTIFSTSSRWSATRHMTYWRGHTIQ	360	

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QY 361 SRPIGGLNTSTHGSTNTSINPRLSPFRSDVYWTESYAGVLLMGYLEPIHGVTVRFN 420
Db 361 SRPIGGLNTSTHGSTNTSINPRLSPFRSDVYWTESYAGVLLMGYLEPIHGVTVRFN 420
QY 421 FRNPQNTFERGTANTSQPYESQGLQKQSETLPPETTERPNYESVSHRSHIGLISQR 480
Db 421 FRNPQNTFERGTANTSQPYESQGLQKQSETLPPETTERPNYESVSHRSHIGLISQR 480
QY 481 VHVVPVSWTHRADRTNTSSISITQIPLVKSFNLSNGTSVVGPGFTGGDIIRTNVNGS 540
Db 481 VHVVPVSWTHRADRTNTSSISITQIPLVKSFNLSNGTSVVGPGFTGGDIIRTNVNGS 540
QY 541 VLSMGLNFNTSLQRYRVRVRAASQTMVLRVTVVGSTTFQGGPSTTSA NESLTSQSR 600
Db 541 VLSMGLNFNTSLQRYRVRVRAASQTMVLRVTVVGSTTFQGGPSTTSA NESLTSQSR 600
QY 601 FAEPFVGISAGSQTAGISISNNAGRTQTFHFKIEFIPITATFAEYDLERAQAVNALP 660
Db 601 FAEPFVGISAGSQTAGISISNNAGRTQTFHFKIEFIPITATFAEYDLERAQAVNALP 660
QY 661 TWTNPRRLKTDVTDHIDOVSNLACLSDPCLDEKRELLEKVKYAKRLSDERNLLQDPN 720
Db 661 TWTNPRRLKTDVTDHIDOVSNLACLSDPCLDEKRELLEKVKYAKRLSDERNLLQDPN 720
QY 721 FTSINKQPDFISTNEQSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFNECY 780
Db 721 FTSINKQPDFISTNEQSNFTSIHQSEHGWGSENITIQEGNDVFKENYVTLPGTFNECY 780
QY 781 PTYLKYKIGSELKAYTRYQIRGYIEDSQDLIEYLIRYNAKHETLDVPGTESVWPLSVES 840
Db 781 PTYLKYKIGSELKAYTRYQIRGYIEDSQDLIEYLIRYNAKHETLDVPGTESVWPLSVES 840
QY 841 PIGRCGEFNRCAPFENWPNDDCSRDGEKCAHSHHPSLDIDIGCTDLHENLGVWVFK 900
Db 841 PIGRCGEFNRCAPFENWPNDDCSRDGEKCAHSHHPSLDIDIGCTDLHENLGVWVFK 900
QY 901 IKTOEGHARLGNLFIEBKPLLGALSRVKAEEKKRDREKLETKRVYVTEAKEAVDA 960
Db 901 IKTOEGHARLGNLFIEBKPLLGALSRVKAEEKKRDREKLETKRVYVTEAKEAVDA 960
QY 961 LFVDSQYNRLQADTNIGMHAADKLVRIRIAYLSELVPGVNAEIFELEGRIITAIS 1020
Db 961 LFVDSQYNRLQADTNIGMHAADKLVRIRIAYLSELVPGVNAEIFELEGRIITAIS 1020
QY 1021 LYDARNVYXGDFNNGLACVNVKGVHVQOQSHRSVLVPIPEWEAEVSQAVRVCPRGYIL 1080
Db 1021 LYDARNVYXGDFNNGLACVNVKGVHVQOQSHRSVLVPIPEWEAEVSQAVRVCPRGYIL 1080
QY 1081 RVTAYKEGEGGCYTHIEIENNTDELKPKNCEBEEVYPTDTGTCNDYTAHQGTAVCNERN 1140
Db 1081 RVTAYKEGEGGCYTHIEIENNTDELKPKNCEBEEVYPTDTGTCNDYTAHQGTAVCNERN 1140
QY 1141 AGYEDAYEVDTTASVNYKPYEETVTDVRRDNHCEYDRGVYVNPPLPAGYVTKLEYEFP 1200
Db 1141 AGYEDAYEVDTTASVNYKPYEETVTDVRRDNHCEYDRGVYVNPPLPAGYVTKLEYEFP 1200
QY 1201 ETDKWTIEIGETGTFIVDSVLELLMEE 1228
Db 1201 ETDKWTIEIGETGTFIVDSVLELLMEE 1228
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RESULT 2

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US-08-448-170-8
; Sequence 8, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narya, Kenneth E.
; APPLICANT: Steiman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
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; TITLE OF INVENTION: B.t. PSI58C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-8
;
; Query Match 91.5%; Score 5926.5; DB 1; Length 1227;
; Best Local Similarity 91.8%; Pred. No. 0;
; Matches 1129; Conservative 36; Mismatches 60; Indels 5; Gaps 3;
;
; QY 1 LTSNRKNEINEINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
; Db 1 LTSNRKNEINEINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
; QY 61 NIAGRIILGVLPVFPAGQATSFYSLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
; Db 61 NIAGRIILGVLPVFPAGQATSFYSLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
; QY 121 LARLQGLGDSFRAYQOQSLDLEWLNRRDDARTSRVLYTOVIALELDPLNAMPFLAIRNQSRP 180
; Db 121 LARLQGLGDSFRAYQOQSLDLEWLNRRDDARTSRVLYTOVIALELDPLNAMPFLAIRNQSRP 180
; QY 181 LLMVYQAANLHLLLRDASLFGSEFGLTSGEIQRYRYERQVQETRDYSDYCVWYNTGLN 240
; Db 181 LLMVYQAANLHLLLRDASLFGSEFGLTSGEIQRYRYERQVQETRDYSDYCVWYNTGLN 240
; QY 241 SLRGTNAASWRYNQFRDLTLGVLDLVALPSPSYDTRTPINTSAQLTREYVTTAIGATG 300
; Db 241 SLRGTNAASWRYNQFRDLTLGVLDLVALPSPSYDTRTPINTSAQLTREYVTTAIGATG 300
; QY 301 V--NMASTNNYNNAPSFAIETAVIRSPHLLDLEQLTIFSTSSRSRATRHMTYWRGHT 358
; Db 301 APSGFASSTNNFNNAAPSFAIETAVIRSPHLLDLEQLTIFSTSSRSRATRHMTYWRGHT 358
; QY 359 IQSPRIQGGNTSTHGSTNTSINPRLSPFRSDVYWTESYAGVLLMGYLEPIHGVTVR 418
; Db 359 IQSPRIQGGNTSTHGSTNTSINPRLSPFRSDVYWTESYAGVLLMGYLEPIHGVTVR 418
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Db 361 LBSRTIRGSLSTHGTNTNTINPVLTQFTSRDVRTSFAGINI--LITTPVNGVPWAR 418
Qy 419 FNFRPONTFEGTANYOPYESPGLOKSDSTELPPTETTERPNYESXSHRLSHGLLSQ 478
Db 419 FNRWPLNSL-RGSLYITGYGVGTQLPDSSTELPPTETTERPNYESXSHRLSNRLLSG 477
Qy 479 SRVHPVSWTHRSADRTNTISDSTIQIPLVKSFNLSNGTSVWSGPGTGGDIIRTNVN 538
Db 478 NTLRAPVSWTHRSADRTNTISDSTIQIPLVKSFNLSNGTSVWSGPGTGGDIIRTNVN 537
Qy 539 GSVLSGFLNFTNSLQRYRVRYAASQTMVLRVTVGSTTDDQFPSTMSANESLTSQS 598
Db 538 GSVLSGFLNFTNSLQRYRVRYAASQTMVLRVTVGSTTDDQFPSTMSANESLTSQS 597
Qy 599 FFAFAPPPVGISASGSGTAGISNNAGROTFFDKIEPIPTATFEAEYDLERAEAVNA 658
Db 598 FFAFAPPPVGISASGSGTAGISNNAGROTFFDKIEPIPTATFEAEYDLERAEAVNA 657
Qy 659 LFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 718
Db 658 LFTNTNPRRLKTDVTDYHIDEVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 717
Qy 719 PNFTSINKQDPDISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVPKENYVTLPGTFNE 778
Db 718 PNFTSINKQDPDISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVPKENYVTLPGTFNE 777
Qy 779 CYPITYLYOKIGSELKAYTRYQLRGVIEDSQLEIYLYRYNAKHETLDVPGTESVWPLSV 838
Db 778 CYPITYLYOKIGSELKAYTRYQLRGVIEDSQLEIYLYRYNAKHETLDVPGTESVWPLSV 837
Qy 839 ESPIGRCGEPNRCAPHFENWPDLCSCRDGKCAHSHHFSLDIDIGCTDLHENLGVWV 898
Db 838 ESPIGRCGEPNRCAPHFENWPDLCSCRDGKCAHSHHFSLDIDIGCTDLHENLGVWV 897
Qy 899 PKIKTQEGHARLGNLEFIEBEKPLLEALSRVRAEKWRDKREKLOLETYRVYTRAKAV 958
Db 898 PKIKTQEGHARLGNLEFIEBEKPLLEALSRVRAEKWRDKREKLOLETYRVYTRAKAV 957
Qy 959 DALFVDSQVNRLOADTNGIMHAADKLVRHIREAYLSVLPVGNABIFEELEGRITTA 1018
Db 958 DALFVDSQVNRLOADTNGIMHAADKLVRHIREAYLSVLPVGNABIFEELEGRITTA 1017
Qy 1019 ISLYDARNVKNKGNDFNNGLACNNVGHVDVQOSHRSVLVPEWEAEVSVQAVRVCPRGY 1078
Db 1018 ISLYDARNVKNKGNDFNNGLACNNVGHVDVQOSHRSVLVPEWEAEVSVQAVRVCPRGY 1077
Qy 1079 ILRVTAKEGYEGCVTHIEIENNTDELKFKNCEEEVYPTDTGTCNDYTAHQGTAVCN 1138
Db 1078 ILRVTAKEGYEGCVTHIEIENNTDELKFKNCEEEVYPTDTGTCNDYTAHQGTAVCN 1137
Qy 1139 RNAGYEDAYEVDTTASVNYKPYEETVTDVRDNHCEYDRGVVNYVPLPAGYMTKELEY 1198
Db 1138 RNAGYEDAYEVDTTASVNYKPYEETVTDVRDNHCEYDRGVVNYVPLPAGYMTKELEY 1197
Qy 1199 PPTDKWIEIGETEGKPIVDSVELLMEE 1228
Db 1198 PPTDKWIEIGETEGKPIVDSVELLMEE 1227

RESULT 3
US-08-961-803-9
; Sequence 9, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-9

Query Match 91.5%; Score 5926.5; DB 3; Length 1227;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1129; Conservative 36; Mismatches 60; Indels 5; Gaps 3;

Qy 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db 1 LTSNRKNEIINALSIPAVSNHSAQNNLSTDAIEDSLCIAEGNNIDPPFVSASTVQTGI 60
Qy 61 NIAGRIILGVLPAGQIASFYSLVGLWPRGRDQWEIFLEHVQLINQITENARNTA 120
Db 61 NIAGRIILGVLPAGQIASFYSLVGLWPRGRDQWEIFLEHVQLINQITENARNTA 120
Qy 121 LARLQGLGDSFRAYCOQSLDNLNRRDARTSVLTQVIALELDFLNAMPLFAIRNQEV 180
Db 121 LARLQGLGDSFRAYCOQSLDNLNRRDARTSVLTQVIALELDFLNAMPLFAIRNQEV 180
Qy 181 LLMVYAQANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWEVNTGLN 240
Db 181 LLMVYAQANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWEVNTGLN 240
Qy 241 SLRGTNAASVRYNQFRRLDLTLGLVDLVALPFSYDTRTYPIINTSAQLTRFVYTDAGTG 300
Db 241 SLRGTNAASVRYNQFRRLDLTLGLVDLVALPFSYDTRTYPIINTSAQLTRFVYTDAGTG 300
Qy 301 V--NWASNNWNNAPSESALETAVIRSPHLLDPLEQLTIFSTSRWSATRHMTVWRGHT 358
Db 301 APSGFASNTWNNNAPSESALAAVIRPPHLLDPEQLTIFSVLSRWSNTQMTNWWVGH 360
Qy 359 IQSRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVVWVWTSYAGVLLWGIYLPBPIHGVPTVR 418
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Db	898	PKIKTQSGHARLGNLEPIEEKPLIGEALSRVKRAEKWKDRKREKLOLETTGRVVTAEKAV	957
Qy	959	DALFVDSQYNRLQADTWNGIMHAADKLVRHIREAYLSELSVIPGVNAIEFEELEGRITTA	1018
Db	958	DALFVDSQYDELQADTWNGIMHAADKLVRHIREAYLSELSVIPGVNAIEFEELEGRITTA	1017
Qy	1019	ISLYDARNVKNQGFNNGLACWNKVGHDVQOQSHRSVLVPIPEWAEVSQAVRVCPRGY	1078
Db	1018	ISLYDARNVKNQGFNNGLACWNKVGHDVQOQSHRSVLVPIPEWAEVSQAVRVCPRGY	1077
Qy	1079	ILRVTAYKEGVEGCVTIHEIENNTDELKPKNCEEEVYPTDGTGTCNDYTAHQGTAVCNS	1138
Db	1078	ILRVTAYKEGVEGCVTIHEIENNTDELKPKNCEEEVYPTDGTGTCNDYTAHQGTAVCNS	1137
Qy	1139	RNAGVEDAYEVDVTASVNYKPTPEEYTYTDVRRDNHCEYDRGVVNPPLPAGYMTKLEY	1198
Db	1138	RNAGVEDAYEVDVTASVNYKPTPEEYTYTDVRRDNHCEYDRGVVNPPLPAGYMTKLEY	1197
Qy	1199	FPETDKVWIEIGETGKPIVDSVELLMEE	1228
Db	1198	FPETDKVWIEIGETGKPIVDSVELLMEE	1227

RESULT 5

US-07-951-715A-7
Sequence 7, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/POCKET NUMBER: S-18805/A/CGC 1577/CIPI

Db 841 RDGEKCAHSHHPSLSDIDVCTDLHENLGVWVVFVKIQTGEGHARLGNLEFIEBEKPLLGBA 900
QY 926 LSRVRAEKWRDKREKQLQLETRKRVYTEAKEAVDALFVDSQYNRLQADTNIGMHAADKL 985
Db 901 LSRVRAEKWRDKREKQLQLETRKRVYTEAKEAVDALFVDSQYDRLOADTNIGMHAADKL 960
QY 986 VHRIRAYLSLSVIPCWNAEIEEELGRIITAIISLYDARNVVGKDFNGLACWNVKXG 1045
Db 961 VHRIRAYLSLSVIPCWNAEIEEELGRIITAIISLYDARNVVGKDFNGLTCWNVKXG 1020
QY 1046 VDVOQSHRSVLVPEWEAEVSQAVRVCPCGRGYILRVTAKEGYGEGCVTTHIEINNTDE 1105
Db 1021 VDVOQSHRSVLVPEWEAEVSQAVRVCPCGRGYILRVTAKEGYGEGCVTTHIEINNTDE 1080
QY 1106 LKFNCEEEVEVPTDGTCTNDYTAHQGT-----VNSNRNAGYEDAYEVDVTTASVNYKPT 1161
Db 1081 LKFNCEEEVEVPTDGTCTNDYTAHQGTAGCADACNSRNAGYEDAYEVDVTTASVNYKPT 1140
QY 1162 EETTYDVRDRDNHCEYDRGVNYPPLPAGYMTKELEYPPETDKWIEIETEGEKPIVDVSV 1221
Db 1141 EETTYDVRDRDNHCEYDRGVNYPPLPAGYMTKELEYPPETDKWIEIETEGEKPIVDVSV 1200
QY 1222 ELLMEE 1228
Db 1201 ELLMEE 1207

RESULT 6

US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent/In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-448A-7

Query Match 87.4%; Score 5659.5; DB 2; Length 1207;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

QY 27 MDLSPDARIEDSLCIAEGNNINPLYSASTVQTGINIAGRIILGVLPFPAGQIASFYSLV 86
Db 1 MDLSPDARIEDSLCIAEGNNIDFFVSASTVQTGINIAGRIILGVLPFPAGQIASFYSLV 60
QY 87 GELWPRGRDQWEIFLEHVEQLINQOITENARNALARLQGLGDSFRAYQOQSLDLENRD 146
Db 61 GELWPRGRDQWEIFLEHVEQLINQOITENARNALARLQGLGDSFRAYQOQSLDLENRD 120
QY 147 DARTRSVLTYQIALELDFLNAMPLFAIRNQVPLMLMYAQAAHLHLLLRDASLFGSEF 206
Db 121 DARTRSVLTYQIALELDFLNAMPLFAIRNQVPLMLMYAQAAHLHLLLRDASLFGSEF 180
QY 207 GLTSQEIQRYERQVEQTRDYSDYCVENYNTGLSLRGNTAASWVRVYQNRDLTLGVLD 266
Db 181 GLTSQEIQRYERQVEQTRDYSDYCVENYNTGLSLRGNTAASWVRVYQNRDLTLGVLD 240
QY 267 LVALPFSYDTRYPTINTSAQLTREVTDAIGATGVNMAWMNNNAPSFAIETAVIRS 326
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Db 301 PHLLDFLEQLTIFSTSSRWASATRWYWRGHTIOSRPIGGGLNTSTHGSTNTSINPVRLS 360
QY 387 PFSRDVYWTESYAGVLLMGILYLEPIHGVTVPFRNPQNTFERGTANYSPYESPGLQL 446
Db 361 FASRDVYWTESYAGVLLMGILYLEPIHGVTVPFRNPQNTFERGTANYSPYESPGLQL 420
QY 447 KDSETELPETTERPNYESYSHRLSHIGLISOSRVHVVPYVSWTHRSADRTNTISDSITQ 506
Db 421 KDSETELPETTERPNYESYSHRLSHIGLISOSRVHVVPYVSWTHRSADRTNTIGPNRITQ 480
QY 507 IPLVKSFNLSGTSVSGPGTGGDIIRTNVNGSVLSMGLNFNTSILQRYVRVRYAASQ 566
Db 481 IPMVKASLPQGTTVARGPGTGGDILRRNTTGGGPIRVTVNGPLQVRVIRGYASTV 540
QY 567 TMLRVTVGSGSTTFDQGFPSSTANESILTSQSFRFAFPVGVISASGSQ-TAGTISINNAG 625
Db 541 DFDFVSRGGTTVNNFRFLTMNSGDELKYNFRRAFTPTFTQIQDITRTISIQLSG 600
QY 626 RQTFHDKIEFIPITATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDVHIQVSNLVA 685
Db 601 NGEVYIDKIEIIPVTAATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDVHIQVSNLVA 660
QY 686 CLSDEFCLDEKRELLEKVKYAKLSDBERNLLOPNFTSINKQPDFISTNEQSNTSIHEQ 745
Db 661 CLSDEFCLDEKRELLEKVKYAKLSDBERNLLOPNFTSINKQPDFISTNEQSNTSIHEQ 720
QY 746 SEHGWMGSENIITIQEGNDVPKENYVTLPGTFNFCYPTLYQKIGESLKYATYQIRGYI 805
Db 721 SEHGWMGSENIITIQEGNDVPKENYVTLPGTFNFCYPTLYQKIGESLKYATYQIRGYI 780
QY 806 EDSQDLIELYLRYNKAKHETLDVPGTSEVMPLSVESPIGRCEPNRCAPHFEWNPDLDCSC 865

Qy 746 SEHGWSGSENIITQEGNDVFNKENVYTLPGTFNCEPTYLYOKIGESSELKAYTRYQLRGYI 805
Db 721 SEHGWSGSENIITQEGNDVFNKENVYTLPGTFNCEPTYLYOKIGESSELKAYTRYQLRGYI 780
Qy 806 EDSODLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRGPNRCAPHFENWPDLDSC 865
Db 781 EDSODLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRGPNRCAPHFENWPDLDSC 840
Qy 866 RDGEKCAHSHHESLDIDIGCTDLHENLGVWVVFVKIQTQEGHARLGNLEFIEBEKPLGEEA 925
Db 841 RDGEKCAHSHHESLDIDIGCTDLHENLGVWVVFVKIQTQEGHARLGNLEFIEBEKPLGEEA 900
Qy 926 LSRVKAERKWRDKREKLEKQLETKRVYTEAKEAVDALFVDSQVNRNLOADTNIGMHAADKL 985
Db 901 LSRVKAERKWRDKREKLEKQLETKRVYTEAKEAVDALFVDSQVNRNLOADTNIGMHAADKL 960
Qy 986 VHRIRAYLSELVPGVNAEIFELEGRHIIITAIISLYDARNVVKNGDFNNGLACVNVKGH 1045
Db 961 VHRIRAYLSELVPGVNAEIFELEGRHIIITAIISLYDARNVVKNGDFNNGLACVNVKGH 1020
Qy 1046 VDVOQSHHRSVLVPEWEAEVSOAVRVCPCRGYILRVYAYKEGCGCTVTHEIENNTDE 1105
Db 1021 VDVOQSHHRSVLVPEWEAEVSOAVRVCPCRGYILRVYAYKEGCGCTVTHEIENNTDE 1080
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Db 1081 LKFKCEBEVYPTDTGTCDNDYTAHOGTAGACACNSRNAGYEDAYEVDVTTASVNYKPTY 1140
Qy 1162 EBETVTDVRRDNHCEYDRGYNYPPLPAGYMTKELEYPEDTKVWIEIGETGKFIVDVSV 1221
Db 1141 EBETVTDVRRDNHCEYDRGYNYPPLPAGYMTKELEYPEDTKVWIEIGETGKFIVDVSV 1200
Qy 1222 ELLLMEE 1228
Db 1201 ELLLMEE 1207

RESULT 8

US-08-459-504B-7
; Sequence 7, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; CORRESPONDENCE ADDRESS: 94
; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459, 504B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459, 595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951, 715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772, 027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-504B-7

Query Match 87.4%; Score 5659.5; DB 3; Length 1207;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;
Qy 27 MDLSDPARIEDSLCTAEGNNINPLVSASTVGTGINIAGRIILGVLPVFPAGQIASFYSFLV 86
Db 1 MDLLPDAIEDSLCTAEGNNIDPFVSASTVGTGINIAGRIILGVLPVFPAGQIASFYSFLV 60
Qy 87 GELWPRGRDQWEIFLEHVEQLINQOITENARNTALRLQGLGDSFRAYQOSLEWLENRD 146
Db 61 GELWPRGRDQWEIFLEHVEQLINQOITENARNTALRLQGLGDSFRAYQOSLEWLENRD 120
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Db 121 DARTSRVLYTQYIALELDPLNAPLFAIRNOEVLPMVYQAANLHLLLRDASLFGSEF 180
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Db 181 GLTSQEIORYYERQVETRDYSDYCVEMWYNTGLNSLRGTNAASWVRYNQFRDITLGVLD 240
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Qy 327 PHLLDELEOLTIFSTSRWSATRMHTYWRGHTTQSRPIGGGLNTSTHGNTNTSINPVRLS 386
Db 301 PHLLDELEOLTIFSTSRWSATRMHTYWRGHTTQSRPIGGGLNTSTHGNTNTSINPVRLS 360
Qy 387 FFSDRVYWTESYAGVLLWGIYLEPIHGVPTVRNFRNPONTFERGTANYSQPESPLQL 446
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Qy 447 KDSETELPPTTERPNYESYSHRLSHGLISQSRVHPVYVSWTHRSADRTNTTSSDSITQ 506
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Db 481 IPWKASELPQGTIVVRGPGFTGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRVRAASQ 540
Qy 567 TMVLRTVVGSTFTDQGPSTMSANBSLTSQSFRAEFVFGISASGSQ-TAGISISNNAG 625
Db 541 DFDFFVSRGGTIVNNFRFLRTMNSGDELKYGVRRAFTTPTFTQIQDIIRTSIQGLSG 600
Qy 626 RQTFHFQKIEFIPITATFEAYDLEAQEAVALFTNTNPRILKTDVTDYHIDQVSNLVA 685

601 NGEVVIDKIBIIPVATFEAYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVA 660
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661 CLSDFCLDEKELEKVKYAKRLSDERNLLQDPNFTSINKDPDISTNEQSNFTSIHQ 720
746 SHGWGSGENITIOBGNDFKKNYVTLPGTFNECYPTLYKIGSELSKAYTRYQLRGYI 805
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841 RDEKCAHSHHFSLDIDIGCTDLHENLGWVWVFKIKTOEGHARLGNLEFTEKPLLGEA 900
926 LSRVRAEKKWRDKREKQLETKRVYVTEAKEAVDALFVDSQVNRLOADNTNIGMIHAADKL 985
901 LSRVRAEKKWRDKREKQLETKRVYVTEAKEAVDALFVDSQVNRLOADNTNIGMIHAADKL 960
986 VRIREAVYLSLSESVIPGVNAEIFELEGGHIIITAIISLYDARNVVKGDFFNGLTCWNVKXH 1045
961 VRIREAVYLSLSESVIPGVNAEIFELEGGHIIITAIISLYDARNVVKGDFFNGLTCWNVKXH 1020
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1106 LKPKNCEBEEVPTDGTGTCNDYTAHQGTA----VCNSRNAGYEDAYEDVDTTASVNYKPTY 1161
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1162 BEETVTVRRDNHCEYDRGYNYPPLPAGYMTKELEYFETDKWIBETGEGKFIYDSV 1221
1141 BEETVTVRRDNHCEYDRGYNYPVPVAGYVTKLEYFETDKWIBETGEGKFIYDSV 1200
1222 ELLLMEE 1228
1201 ELLLMEE 1207

RESULT 9
US-08-459-444-7

Sequence 7, Application US/08459444A
Patent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launig, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/PI/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-459-444-7

Query Match 87.4%; Score 5659.5; DB 3; Length 1207;

Best Local Similarity 89.4%; Pred. No. 0;

Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

QY 27 MDLSPDARIEDSLCIAEGNNINPLVSASTVGTGINIAGRILGLVGLVPPAGQIASPYSFLV 86
DB 1 MDLSPDARIEDSLCIAEGNNIDPPVSASTVGTGINIAGRILGLVGLVPPAGQIASPYSFLV 60
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QY 147 DARTRSVLTYQYIALELDPLNAMPFAIRNOVEPLLMVYAOANLHLLLRDASLFGSEF 206
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DB 421 KOSTELPPETTERPNYESYSHRLSHIGLSOSRVHPVYVSWTHRSADRTNITSDSITQ 480
QY 507 IPLVKSFNLSNGTSVWSGPGTGDIITRTNVGSLNGLNFNTSLQRYVRVRYAASQ 566
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QY 567 TMLRVTVGGSTTFDQGFPPSTMSANESLTSQSPFAEFPGVIGISAGSQ-TAGISISNNAG 625
DB 541 DFDFFVSRRGGTTVNNPRFLRTMNSGDELKYNFVRAFTTPTFTQIQDIIRTSIQGLSG 600
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DB 601 NGEVVIDKIBIIPVATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 660

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Db 661 CLSDFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHQ 720
Qy 746 SEHGWSGSENIITQEGNDVFKENYVTLPGTFNFCYPTLYQKIGESLKYTRYQLRGYI 805
Db 721 SEHGWSGSENIITQEGNDVFKENYVTLPGTFNFCYPTLYQKIGESLKYTRYQLRGYI 780
Qy 806 EDSQDLIYLIRYNAKHETLDVFGTSEVWPLSVESPIGRGCEPNRCAPHFENPDLDCSC 865
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Qy 866 RDEKCAHSHHFLSDIDIGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEEKLGEA 925
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Qy 926 LSRVKAERKWRDKREKLETKRVVTEAKEAVDALFVDSQYDRLOADTNIGMHAADKL 985
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Qy 1222 ELLMEE 1228
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RESULT 10
US-09-053-549-8
; Sequence 8, Application US/09053549
; Patent No. 6121521
; GENERAL INFORMATION:
; APPLICANT: Desat, Nalini
; TITLE OF INVENTION: No. 6121521e1 Insecticidal Protein and Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: No. 6121521artis Corporation
; STREET: 3054 Cornwalis Rd.
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,549
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-053-549-8
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Query Match      87.4%; Score 5659.5; DB 3; Length 1207;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;
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Qy 27 MDLSPDARIEDSICIAEGNNINPLVSASTVQTGINIAGRIILGVLPVFPAGQIASFSFLV 86
Db 1 MDLLPDARIEDSICIAEGNNIDPFVSASTVQTGINIAGRIILGVLPVFPAGQIASFSFLV 60
Qy 87 GELWPRGRDOMEIPLFHEVQELINQOITENARNTALARLQGLGDSFRAYQOQSLDLENRD 146
Db 61 GELWPRGRDOMEIPLFHEVQELINQOITENARNTALARLQGLGDSFRAYQOQSLDLENRD 120
Qy 147 DARTSRVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEF 206
Db 121 DARTSRVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEF 180
Qy 207 GLTSQEIQRVYERQVETRDYSDYCVWYNTGLNSLRGTNAASWVRYNQFRDLTLGVLD 266
Db 181 GLTSQEIQRVYERQVETRDYSDYCVWYNTGLNSLRGTNAASWVRYNQFRDLTLGVLD 240
Qy 267 LVALPFSYDTRYPINTSAQLTRVYVTDGATGVNMAWMYNNAPSFSAIEAAIRS 326
Db 241 LVALPFSYDTRYPINTSAQLTRVYVTDGATGVNMAWMYNNAPSFSAIEAAIRS 300
Qy 327 PHLLDFLEOLITFTSSRWSATRHMYRGHTIQSRPIGGGLNTSTHGSTNTSINPRLS 386
Db 301 PHLLDFLEOLITFTSSRWSATRHMYRGHTIQSRPIGGGLNTSTHGSTNTSINPRLS 360
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Qy 447 KDSETELPETTERPNYESYSHRLSHIGLISQSRVHVVPVYSWTHRSADRTNTTISDSITQ 506
Db 421 KDSETELPETTERPNYESYSHRLSHIGLISQSRVHVVPVYSWTHRSADRTNTTISDSITQ 480
Qy 507 IPLVKSENLNGTSSVSGPGTGGDIIRTNVNGSVLSMGLNFNTSILQRYRVRYAASQ 566
Db 481 IPWKASELPGTTVVRGPGTGGDIIRTNVNGSVLSMGLNFNTSILQRYRVRYAASQ 540
Qy 567 TWVLRVTVGGSTTFDQGPPTMSANESLTSQSFRAEFVPGVSGISAGSQ-TAGISISNAG 625
Db 541 DFDFFVSRGGTTVANNFRPLRTMNSGDELKYGNFVRRATFTPTFQIQDIRTSIQLSG 600
Qy 626 RQTFHEDKIEPIPTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDVHIDQVSNLVA 685
Db 601 NGEVTDKIEIIPVTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDVHIDQVSNLVA 660
Qy 686 CLSDFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHQ 745
Db 661 CLSDFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHQ 720
Qy 746 SEHGWSGSENIITQEGNDVFKENYVTLPGTFNFCYPTLYQKIGESLKYTRYQLRGYI 805
Db 721 SEHGWSGSENIITQEGNDVFKENYVTLPGTFNFCYPTLYQKIGESLKYTRYQLRGYI 780
Qy 806 EDSQDLIYLIRYNAKHETLDVFGTSEVWPLSVESPIGRGCEPNRCAPHFENPDLDCSC 865
Db 781 EDSQDLIYLIRYNAKHETLDVFGTSEVWPLSVESPIGRGCEPNRCAPHFENPDLDCSC 840
Qy 866 RDEKCAHSHHFLSDIDIGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEEKLGEA 925
Db 841 RDEKCAHSHHFLSDIDIGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEEKLGEA 900
Qy 926 LSRVKAERKWRDKREKLETKRVVTEAKEAVDALFVDSQYDRLOADTNIGMHAADKL 985
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Db 901 LSRVRAEKWKDKREKLETKRVVTEAKEAVDALFVDSQYDRLOQADTNIGMIIHAADKL 960
QY 986 VHRIRAYLSLSVPGVNAEIPFEELGRITTAISLYDARNVVGKDFNGLACVNVKGH 1045
Db 961 VHRIRAYLSLVPVGVNAEIPFEELGHIITTAISLYDARNVVGKDFNGLTCNVKGH 1020
QY 1046 VDVOQSHRSVLVPEWEAEVQAVRVCPRGYILRVTAAYKEGYGEGCVTIHEIENNTDE 1105
Db 1021 VDVOQSHRSVLVPEWEAEVQAVRVCPCGYILRVTAAYKEGYGEGCVTIHEIENNTDE 1080
QY 1106 LFKKCEBEVEVPTDGTGNDYTAHQGTGTA- ---VCNSRNAGYEDAYEVDVTTASVNVKPTY 1161
Db 1081 LFKKCEBEVEVPTDGTGNDYTAHQGTAGACADACNSRNAGYEDAYEVDVTTASVNVKPTY 1140
QY 1162 EBETVTDVRDNHCEYDRGVNYPPLPAGYMTKELEYFPETDKVWIEIGETGKFIIVDSV 1221
Db 1141 EBETVTDVRDNHCEYDRGVNYPVPVAGYVTKLEYFPETDVWIEIGETGKFIIVDSV 1200
QY 1222 ELLLMEE 1228
Db 1201 ELLLMEE 1207

RESULT 11

US-09-547-422-7
; Sequence 7, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Korziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-547-422-7

Query Match 87.4%; Score 5659.5; DB 3; Length 1207;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;
QY 27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRILGLVGPVAGQIASYPSFLV 86
Db 1 MDLSPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRILGLVGPVAGQIASYPSFLV 60
QY 87 GELPRGRDQWEIIFLEHVQQLINQOITENARNTALARIQGLGDSFRAYCOOSLEDWLENRD 146
Db 61 GELPRGRDQWEIIFLEHVQQLINQOITENARNTALARIQGLGDSFRAYCOOSLEDWLENRD 120
QY 147 DARTSRVLYTQYIALELDPLNAMPLFAIRNOEVPLLMVYQAANLHLLLRDASLFGSEF 206
Db 121 DARTSRVLYTQYIALELDPLNAMPLFAIRNOEVPLLMVYQAANLHLLLRDASLFGSEF 180
QY 207 GLTSGEIQRYRQVQETRDYSDYCEWYNTGLNSLRCTNAASWRYNQFRDRLTLGVLD 266
Db 181 GLTSGEIQRYRQVQETRDYSDYCEWYNTGLNSLRCTNAASWRYNQFRDRLTLGVLD 240
QY 267 LVALPPSYDTRTYPTINTSAQLTREYVTDATCATGVNMAWVWYNNNAPSAIETAVIRS 326
Db 241 LVALPPSYDTRTYPTINTSAQLTREYVTDATCATGVNMAWVWYNNNAPSAIETAAIRS 300
QY 327 PHLLDFLEQLTIFSTSSRWSSATRMWYRGHTIOSRPICGGGLNTSTHGSTNTSINPVRLS 386
Db 301 PHLLDFLEQLTIFSSASRWSSATRMWYRGHTIOSRPICGGGLNTSTHGSTNTSINPVRLS 360
QY 387 FFSRDVWYTESYAGVLLMGVILEPIHGVPVTRFNPNQNTFERTGANTYSPYSPGLQL 446
Db 361 FASRDVWYTESYAGVLLMGVILEPIHGVPVTRFNPNQNTSDRGNTYSPYSPGLQL 420
QY 447 KDSLETLPETTERPNYESYSHRLSHIGLISQSRVHVVPVYSWTHRSADRTNTISDSITQ 506
Db 421 KDSLETLPETTERPNYESYSHRLSHIGLISQSRVHVVPVYSWTHRSADRTNTIGENRITQ 480
QY 507 IPLVKSNLNSGTSVWSGPGTGDIIITNVNGSVLSMGLNFNNTSLQRYRVRVYAAASQ 566
Db 481 IPWKASLPQGTTVVRGPGTGDILRRWTGFGPIRVTVNGPLTQRYAIGFYASTV 540
QY 567 TMLRVTVGSGTTFDQGPSTMSANESLTSQSFPAEFVPGISASGSQ-TAGISISNNAG 625
Db 541 DFDFVSRGGTTVANNFRPLRTMNSGDELKYGNFVRRAPTTPFTTQIQDIIRTSIQGLSG 600
QY 626 RQTFHFKIEIPITATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 685
Db 601 NGEYVYDKIEIIPVTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVA 660
QY 686 CLSDFECLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKOPDFISNEQSNFTSIHEQ 745
Db 661 CLSDFECLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKOPDFISNEQSNFTSIHEQ 720
QY 746 SEHGWSGSENIITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESLKYATRYQLRGYI 805
Db 721 SEHGWSGSENIITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESLKYATRYQLRGYI 780
QY 806 EDSQDLIELYLRVNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHPFWNPDLDSCC 865
Db 781 EDSQDLIELYLRVNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHPFWNPDLDSCC 840
QY 866 RDGEKCAHSHHSLDIDIGCTDLHENLGVWVWFKITQEGHARLGNLEFTEEPKPLGEA 925
Db 841 RDGEKCAHSHHSLDIDVGCTDLHENLGVWVWFKITQEGHARLGNLEFTEEPKPLGEA 900
QY 926 LSRVRAEKWKDKREKLETKRVVTEAKEAVDALFVDSQYDRLOQADTNIGMIIHAADKL 985

Db 901 LSRVGAERKWRDKREKLEQLETKRVVTEAKEAVDALFVDSQVDRLOADTNIGMHAADKL 960
QY 986 VHRIRAYLSELVPIGVNAEIPPELEGRITTAISLYDARNVVGXGDFNNGLACWNVKGH 1045
Db 961 VHRIRAYLSELVPIGVNAEIPPELEGRITTAISLYDARNVVGXGDFNNGLTCWNVKGH 1020
QY 1046 VDVOQSHRSVLVPIPWEAEVSOAVRVCGRGVYILRVATYKGYGEGCVTTHEIENNTDE 1105
Db 1021 VDVOQSHRSVLVPIPWEAEVSOAVRVCGRGVYILRVATYKGYGEGCVTTHEIENNTDE 1080
QY 1106 LKPKNCEBEVPTDGTGTCNDYTAHQGTGTA---VCNSRNAGYEDAYEVDVTTASVNNKPTY 1161
Db 1081 LKPKNCEBEVPTDGTGTCNDYTAHQGTGACADACNSRNAGYEDAYEVDVTTASVNNKPTY 1140
QY 1162 EBETTYDVRDNHCEYDRGVNYPPLPAGYMTKELEYPPETDKWIEIGETGKPIVDSV 1221
Db 1141 EBETTYDVRDNHCEYDRGVNYPVPAGYVTKLEYPPETDVTWIEIGETGKPIVDSV 1200
QY 1222 ELLMEE 1228
Db 1201 ELLMEE 1207

RESULT 12

US-09-988-462-7

Sequence 7, Application US/09988462

Patent No. 6720488

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwalis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-No. 6720488-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-988-462-7

Query Match 87.4%; Score 5659.5; DB 4; Length 1207;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1079; Conservative 34; Mismatches 89; Indels 5; Gaps 2;

QY 27 MDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRLGVLPAGQATASFVSFLV 86
Db 1 MDLSPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRLGVLPAGQATASFVSFLV 60
QY 87 GELWPRGRDQWEIFLEHVEQLINQITENARTALARLQGLGDSFRAYQQSLEDWLENRD 146
Db 61 GELWPRGRDQWEIFLEHVEQLINQITENARTALARLQGLGDSFRAYQQSLEDWLENRD 120
QY 147 DARTSRVLYTOYIALELDFLNAMPLFAIRNQEVPLLMVYAAANLHLLLRDASLFGSEF 206
Db 121 DARTSRVLYTOYIALELDFLNAMPLFAIRNQEVPLLMVYAAANLHLLLRDASLFGSEF 180
QY 207 GLTSQEIQRYERQVEQTRDYSYCVWYNTGLNSLRGTNAASWVRYNQFRDLTLGVLD 266
Db 181 GLTSQEIQRYERQVEQTRDYSYCVWYNTGLNSLRGTNAASWVRYNQFRDLTLGVLD 240
QY 267 LVALPSPDYTRYPINTSAQLTRVYTDAGATGVNMAWMYNNAPSFSAIETAVIRS 326
Db 241 LVALPSPDYTRYPINTSAQLTRVYTDAGATGVNMAWMYNNAPSFSAIETAVIRS 300
QY 327 PHLLDFLEQLTIFSTSSRWASATRHMTYWRGHTIQSRPIGGGLTSTHGSTNTSINPVLRS 386
Db 301 PHLLDFLEQLTIFSTSSRWASATRHMTYWRGHTIQSRPIGGGLTSTHGSTNTSINPVLRS 360
QY 387 FFSRDVYNTESYAGVLLMGVILEPIHGVTYPRNFNPQNTFERGTANYSPYSPGQL 446
Db 361 FASRDVYNTESYAGVLLMGVILEPIHGVTYPRNFNPQNTFERGTANYSPYSPGQL 420
QY 447 KDSETELPETTERENYSHLSHIGLIQSQRVHVVPVYSWTHRSADRTTISDSITQ 506
Db 421 KDSETELPETTERENYSHLSHIGLIQSQRVHVVPVYSWTHRSADRTTIGENRITQ 480
QY 507 IPLVKSFNLSGTSVVGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYRVRYAAASQ 566
Db 481 IPMVKASELPQGTTVVRGPGFTGGDILRRNTWTGFGPIRVTVNGPLTQRYIGFYASTV 540
QY 567 TMLRVTVGSGTTPDQGPSTMSANESLTSQSPFAEPFVGISASGQ-TAGISINNAG 625
Db 541 DFDVFSRGGTIVNFRFLRTMNSGDELKYGNFVRAFTTPTFTQIQDIIRTSIQGLSG 600
QY 626 RQTFHFDKIEFIPITATPEAEYDLERAQEAVALFTNTNPRRLKTDVTHIDOVSNLVA 685
Db 601 NGEVYIDKIEIIPVATPEAEYDLERAQEAVALFTNTNPRRLKTDVTHIDOVSNLVA 660
QY 686 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIEHQ 745
Db 661 CLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIEHQ 720
QY 746 SEHGWWGSENITIOEGNDVFKENVVTLPGTFNECYPTLYKIGESLKYATRYQLRGYI 805
Db 721 SEHGWWGSENITIOEGNDVFKENVVTLPGTFNECYPTLYKIGESLKYATRYQLRGYI 780
QY 806 EDSQDLBIYLRVNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFEPWPDLDSCS 865
Db 781 EDSQDLBIYLRVNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFEPWPDLDSCS 840
QY 866 RDGEKCAHSHHSLDIDIGCTDLHENLGYVWVFKIKTQEGHARLGNLEFIEBKPLLGEA 925
Db 841 RDGEKCAHSHHSLDIDIGCTDLHENLGYVWVFKIKTQEGHARLGNLEFIEBKPLLGEA 900

QY 926 LSRVKAERKWRDREKLEKLETRKRVYTEAKEAVDALFVDSQYNRLQADTNGIHAADKL 985
DB 901 LSRVKAERKWRDREKLEKLETRKRVYTEAKEAVDALFVDSQYDRQLQADTNGIHAADKL 960
QY 986 VHRIRAYLSELSVIGVNAEIPFEELEGRITTAISLYDARNVVKGD FNGLA CNVKGH 1045
DB 961 VHRIRAYLSELSVIGVNAEIPFEELEGHITTAISLYDARNVVKGD FNGNGLTCWNVKGH 1020
QY 1046 VDVOQSHRSVLVPEWEAEVSAVRVCPGRGYILRVTA YKEGYGEGCVTIHEIENNTDE 1105
DB 1021 VDVOQSHRSVLVPEWEAEVSAVRVCPGRGYILRVTA YKEGYGEGCVTIHEIENNTDE 1080
QY 1106 LKFKNCEBEVPTDGTGTCNDYTAHQGTA----VCNSRNAGYEDAYEVDVTTASVNYKPTY 1161
DB 1081 LKFKNCEBEVPTDGTGTCNDYTAHQGTAGCADCNSRNAGYEDAYEVDVTTASVNYKPTY 1140
QY 1162 ESETYDVRDNHCEYDRGVNVPPLPAGYMKELFPPETDKWIEIGETGKPIVDSV 1221
DB 1141 ESETYDVRDNHCEYDRGVNVPVPGYVTKELFPPETDKWIEIGETGKPIVDSV 1200
QY 1222 ELLLMEE 1228
DB 1201 ELLLMEE 1207

RESULT 13

US-09-053-549-2
; Sequence 2, Application US/09053549
; Patent No. 6121521
; GENERAL INFORMATION:
; APPLICANT: Desai, Nalini
; TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: No. 6121521artis Corporation
; STREET: 3054 Cornwalis Rd.
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,549
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1227 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-053-549-2

Query Match 83.9%; Score 5436.5; DB 3; Length 1227;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 1040; Conservative 63; Mismatches 118; Indels 13; Gaps 5;

QY 1 LTSNRKNEINLALSIPAVNHSHTQMDLSPDARTEDSLCIAEGNNINPLVSASTVQTGI 60
DB 1 MTSNRKNEINL----AVNHSQAQMDLLPDARTEDSLCIAEGNNIDPFVSASTVQTGI 55
QY 61 NIAGRILGLVGPVFAQIASFYSFLVGLWPRGRDQWEIFLHVQLINQQTENARNTA 120

DB 56 NIAGRILGLVGPVFAQLASFYSFLVGLWPRGRDQWEIFLHVQLINQQTENARNTA 115
QY 121 LARLOGLGDSFRAYQOOSLEDWLENRDDARTSVLTQYIALELDFNANPLFAIRNQEV 180
DB 116 LARLOGLGDSFRAYQOOSLEDWLENRDDARTSVLTQYIALELDFNANPLFAIRNQEV 175
QY 181 LLMWYAQAANLHLLLRDASLFGSFGSLTQSOEIQRYERYQVETRDYSDYCVWNTGN 240
DB 176 LLMWYAQAANLHLLLRDASLFGSFGSLTQSOEIQRYERYQVETRDYSDYCVWNTGN 235
QY 241 SLRGTAASWRYNQFRDLTLGLVLDLVALPSPDYDTRTPINTSAQLTREVTDAIGATG 300
DB 236 SLRGTAASWRYNQFRDLTLGLVLDLVALPSPDYDTRTPINTSAQLTREVTDAIGATG 295
QY 301 VNMASMYNNANPSPSAIETAVIRSPHLLDFLEQLTIFSSRSASRHTMYTWGHTIQ 360
DB 296 VNMASMYNNANPSPSAIETAVIRSPHLLDFLEQLTIFSSRSASRHTMYTWGHTIQ 355
QY 361 SRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVMYTESVAGVLLWGIYLEPIHGVTVRPN 420
DB 356 SRPIGGGLNTSTHGSTNTSINPVRLSFFSRDVMYTESVAGVLLWGIYLEPIHGVTVRPN 415
QY 421 FRNPONTFERGTANYSQYSPGSLQKDSSETPELPTTERPNYESYSHRLSHIGLISOSR 480
DB 416 FRNPONTFERGTANYSQYSPGSLQKDSSETPELPTTERPNYESYSHRLSHIGLISOSR 475
QY 481 VHVPUYSWTHESADRTNTISSDSITQIPLVKSFNLSGTSVVGSGPFGGDIIRTNVGS 540
DB 476 VHVPUYSWTHESADRTNTISSDSITQIPLVKSFNLSGTSVVGSGPFGGDIIRTNVGS 535
QY 541 VLSMGLNNTSLQRYRVRVYAAASQTMVLVAVTGVGGSTTFQGGFSTMSANESLTSQSPR 600
DB 536 FGPTRVTVNGPLTQRYRIGPYASTVDFDFVSRGGTTVNNFRFARTWNSGDELKYGHFV 595
QY 601 FAEPPVGISASGQT-AGISINNAGROTFFDKIEFIPITATFAEYDLERAQAVNAL 659
DB 596 RRAFTPTFTQIQNIIRTSIQGLSGNGEVYDKIEIIPVTATFAEYDLERAQAVNAL 655
QY 660 FTNTNPRKLTVDYDHYDQVSNLVACLSDFCLDEKELLEKVKYAKRSLDERLLQDP 719
DB 656 FTNTNPRKLTVDYDHYDQVSNLVACLSDFCLDEKELLEKVKYAKRSLDERLLQDP 715
QY 720 NTSINKQDPFISTNEQSNFTSIHQSEHGHWGSENITIQGNDVFKENYVTLPTFNEC 779
DB 716 NTSINKQDPFISTNEQSNFTSIHQSEHGHWGSENITIQGNDVFKENYVTLPTFNEC 775
QY 780 YPTYLYQKIGSELKAVTRYQLRGYIEDSQDLIYLIRYNKAKHETLDVPGTESVWPLSVE 839
DB 776 YPTYLYQKIGSELKAVTRYQLRGYIEDSQDLIYLIRYNKAKHETLDVPGTESVWPLSVE 835
QY 840 SPIGRGCEPNRCAPHFENPDLCSDRGKCAHSHHSPDLIDIGCTDLHENLGVWVVF 899
DB 836 SPIGRGCEPNRCAPHFENPDLCSDRGKCAHSHHSPDLIDIGCTDLHENLGVWVVF 895
QY 900 KIKTQBGHARLGNLEFTEKPLLEALSRVRAEKWRDKREKLETKRVVTEAKEAVD 959
DB 896 KIKTQBGHARLGNLEFTEKPLLEALSRVRAEKWRDKREKLETKRVVTEAKEAVD 955
QY 960 ALFVDSQYNRLQADTNGIHAADKL VHRIRAYLSELSVIGVNAEIPFEELEGRITTAI 1019
DB 956 ALFVDSQYNRLQADTNGIHAADKL VHRIRAYLSELSVIGVNAEIPFEELEGRITTAI 1015
QY 1020 SLYDARNVVKGD FNGNGLTCWNVKGHVDV--QSHRSVLVTPWEAEVSAVRVCPGRGY 1078
DB 1016 SLYDARNVVKGD FNGNGLTCWNVKGHVDV--QSHRSVLVTPWEAEVSAVRVCPGRGY 1075
QY 1079 ILRVTA YKEGYGEGCVTIHEIENNTDELKFNCEEEVYPTDGTGTCNDYTA---HQGTA 1134
DB 1076 ILRVTA YKEGYGEGCVTIHEIENNTDELKFNCEEEVYPTDGTGTCNDYTA---HQGTA 1134
QY 1135 VCNSRNAGYEDAYEVDVTTASVNYKPTYBEETTYDVRDNHCEYDRGVNVPVPGYVTK 1194

Db 1135 -YTSRNRGCGAYBSNSVPADYASVEEYKAYTDGRRDNPCESNRGVDYTPLPAGYVTK 1193

QY 1195 ELEYFPETDKWIIEIGETEGKFIVDSVELLMEE 1228

Db 1194 ELEYFPETDKWIIEIGETEGTFIVDSVELLMEE 1227

RESULT 14

US-08-100-709-4

; Sequence 4, Application US/08100709

; Patent No. 5322687

; GENERAL INFORMATION:

; APPLICANT: Donovan, William P.

; APPLICANT: Tan, Yiping

; APPLICANT: Jan, Christine S.

; APPLICANT: Gonzalez Jr., Jose M.

; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5

; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

; ADDRESSEE: Nadel

; STREET: 1601 Market Street, 36th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/100,709

; FILING DATE: 19930729

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Egolf, Christopher

; REGISTRATION NUMBER: 27633

; REFERENCE/DOCKET NUMBER: 7205-49

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-757-1590

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1229 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-100-709-4

Query Match 80.8%; Score 5237.5; DB 1; Length 1229;

Best Local Similarity 79.9%; Pred. No. 0;

Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

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Db 61 NIAGRILGVLPVGPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQQITENARNTA 120

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Db 121 LARLQGLGDSFRAYQOQSLDNLNDRDARTSVLYTQYTALELDFLNAPLFAIRNQVEVP 180

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Db 181 LLMYAQAANHLILLRDLASLFGSEFGLTSQEIQRYYRQVEQTRDYSYCVQWNTGLN 240

QY 241 SLRGTNAASWVRNQFRDLTLGLVLDVALFSDYTRTPYINTSAQLTREVTDAIGATG 300

Db 241 SLRGTNAASWVRNQFRDLTLGLVLDVALFSDYTRTPYINTSAQLTREVTDAIGATG 300

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QY 359 IQSRPIGGCLNTSTHGST-NTSINPVRLSPFSRDVWVWTESYAGVLLWGLIYFIHGVPTV 417

Db 361 LNFPIGGTLNTSTOGLTNTSINPVTLQFTSDVWVWTESNAGTNI--LFTTVNGVPMWA 418

QY 418 RFNRPNTFERTGANYSQYSPGLQKDSSETLPPETTERPNYESHRLSHLGLIS 477

Db 419 RFNRPNTFERTGANYSQYSPGLQKDSSETLPPETTERPNYESHRLSHLGLII 478

QY 478 QSRVHVVPVSWTHRSADRTNTISSDSITQIPLVKSFLNLSGTSVSGPGFTGSDIIRTNV 537

Db 479 GNTLRAPVSWTHRSADRTNTIGPNRITQIPLVKSFLNLSGTSVSGPGFTGSDIIRTNV 538

QY 538 NGSVLSMGLNFNNTSLQRYVRVRYAASQTMVLRVTVGGSTTFDQGFPPSTMSANESLTSQ 597

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QY 598 SFRFAEPVPGISASGSOTAGISISNNAGQTHFDKIEFIPITATPEAEYDLERAQEA 657

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Db 1199 YFPETDVWIEIGETEGKFIVDSVELLMEE 1229

RESULT 15

US-08-176-865-4

; Sequence 4, Application US/08176865

; Patent No. 5616319

; GENERAL INFORMATION:

; APPLICANT: Donovan, William P.

; APPLICANT: Tan, Yiping

APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS c1yET4 AND c1yET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSES: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESSES: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,865
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-176-865-4

Query Match 80.8%; Score 5237.5; DB 1; Length 1229;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 983; Conservative 94; Mismatches 149; Indels 5; Gaps 3;

QY 1 LTSNRKNEINIALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNINPLVLSASTVQTGI 60
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QY 301 V--NNASMNWNNAPSASLETAVIRSPHLLDLEQLTIPSTSSRWATRHMTYWRGHT 358
DB 301 APSGFASTWNNAPSASLEAAIFRPHLLDLPPEQLTIYSASRSWSSTQHMNVVGH 360
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DB 361 LNFRPIGGLNTSTOGLTNTSINPVLQTSRDVYRTESNAGTNI--LPTTPVNGVPA 418
QY 418 RPNFRNPONTFRGTANTSQPYESGLQKQSETELPPTTERPNYESYSHRLSHIGLI 477

DB 419 RPNFINQNIYERGATTYSQPYQVGIQLFDPSETELPPTTERPNYESYSHRLSHIGLI 478
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DB 1019 AMSLYDARNVVKNGDFNNGLTCMNVKGVHVQOQSHRSVLVPIPEWAEVSQAVRVCGRG 1078
QY 1078 YILRVATYKEGYGEGCVTIHEIENNTDELKFNCEEEVEYPTDTGTCNDYTAHQGTAVCN 1137
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QY 1138 SRNAGYEDAYEVDTTASVNYKPTVEETTYTVDRDNHCEYDRGVYVYPPAGYVTKLE 1197
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Search completed: November 21, 2004, 17:01:23

Job time : 50 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2004, 16:55:57 ; Search time 113 Seconds
(without alignments)
3848.395 Million cell updates/sec

Title: US-10-614-524-2

Perfect score: 6479

Sequence: 1 LTSNRKNEININLSIPAV.....IGETGKFIVDSVELLMEE 1228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	6464	99.8	1228	14	US-10-428-961-38
3	5912.5	91.3	1227	14	US-10-428-961-63
4	5742	88.6	1228	16	US-10-809-953-10
5	5659.5	87.4	1207	10	US-09-988-462-7
6	5108	78.8	1186	9	US-09-826-660-23
7	3502.5	54.1	1189	14	US-10-200-522-59
8	3502.5	54.1	1189	17	US-10-855-535-59
9	3500.5	54.0	1189	10	US-09-972-175-2
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11	3500.5	54.0	1189	17	US-10-855-535-2
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ALIGNMENTS

RESULT 1

US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match 100.0%; Score 6479; DB 15; Length 1228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	LTSNRKNEININLSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI	60
QY	61	NIAGRILGLVGPFGAQIASFYSLVGLWPRGRDQWEIFLEHVQLINQITENARNTA	120

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Db      421  FRNPQNTFERGTANYSQPYESPGQLKXSETLPPETTERPNYESYSHRLSHIGLISQSR 480
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Db      1021  LYDARNVVKNGDFNGLACVNWVGHVDVQOSSHRSVLVPEWEAEVSOAVRCPGGRGYIL 1080
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Db      1141  AGYEDAVEVDTTASVNYKPYEBETTYDVRDNHCEYDRGVVYVPPPLPAGYMTKELEYFP 1200
Qy      1201  ETDKVMIEIGETEGKFIVDSEVLLMBE 1228
Db      1201  ETDKVMIEIGETEGKFIVDSEVLLMBE 1228

RESULT 2
US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupatz, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38
```

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Query Match      99.8%; Score 6464; DB 14; Length 1228;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1224; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy      1  LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db      1  LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Qy      61  NIAGRILGVLPFAQIASFYSFLGELWPRGRDQWEIFLEHVQLINQOITENARNTA 120
Db      61  NIAGRILGVLPFAQIASFYSFLGELWPRGRDQWEIFLEHVQLINQOITENARNTA 120
Qy      121  LARLOGLGDSFRAYQOQSLDLENRDDRATRSVLTYQYIALELDFLNAMPLFAIRNQVEVP 180
Db      121  LARLOGLGDSFRAYQOQSLDLENRDDRATRSVLTYQYIALELDFLNAMPLFAIRNQVEVP 180
Qy      181  LMVYAQAANLHLLLRDASLFGSEFGLTSQBIQRYRQVEQTRDYSQVWYNTGLN 240
Db      181  LMVYAQAANLHLLLRDASLFGSEFGLTSQBIQRYRQVEQTRDYSQVWYNTGLN 240
Qy      241  SLRGTTNAASWRYNQPRDLTLGVLDLVALFSPSYDTRTPINTSAQLTREYVYDAIGATG 300
Db      241  SLRGTTNAASWRYNQPRDLTLGVLDLVALFSPSYDTRTPINTSAQLTREYVYDAIGATG 300
Qy      301  VNMAAMWNNNAPFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSAATRHMTYWRGHTIQ 360
Db      301  VNMAAMWNNNAPFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSAATRHMTYWRGHTIQ 360
Qy      361  SRPIGGGLNTSTHGSTNTSINPVLSPFSRDVYVWTESYAGVLLAGIYLEPIHGVTYVRFN 420
Db      361  SRPIGGGLNTSTHGSTNTSINPVLSPFSRDVYVWTESYAGVLLAGIYLEPIHGVTYVRFN 420
Qy      421  FRNPQNTFERGTANYSQPYESPGQLKXSETLPPETTERPNYESYSHRLSHIGLISQSR 480
Db      421  FRNPQNTFERGTANYSQPYESPGQLKXSETLPPETTERPNYESYSHRLSHIGLISQSR 480
Qy      481  VHVVPVSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVNGS 540
Db      481  VHVVPVSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVSGPGFTGGDIIRTNVNGS 540
```

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QY 541 VLSMGLNFNTSLQRYRVRVYAAASQTMVLRVTVGSTTFDQGFPTMSANESLTSQSFR 600
DB 541 VLSMGLNFNTSLQRYRVRVYAAASQTMVLRVTVGSTTFDQGFPTMSANESLTSQSFR 600
QY 601 FPAEFPVGISASGSGTAGISINNAGROTTHFKIEPIPTATFEAYDIERAQEAVNALP 660
DB 601 FPAEFPVGISASGSGTAGISINNAGROTTHFKIEPIPTATFEAYDIERAQEAVNALP 660
QY 661 TWTNPRRLKTDVTDYHIDOVSNLVACLDEFCLDEKRELLEKVKYAKRLSDERNLLQDPN 720
DB 661 TWTNPRRLKTDVTDYHIDOVSNLVACLDEFCLDEKRELLEKVKYAKRLSDERNLLQDPN 720
QY 721 FTSINKQPDFISTNEQSNFTSIHQSEHGWGSENIITQEGNDVFKENYVTLPGTFNECY 780
DB 721 FTSINKQPDFISTNEQSNFTSIHQSEHGWGSENIITQEGNDVFKENYVTLPGTFNECY 780
QY 781 PLYLYQKIGESLSEKATRYQLRGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
DB 781 PLYLYQKIGESLSEKATRYQLRGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWPLSVES 840
QY 841 PIGRCGEPRNRCAPHFENWPDLCSCRDGKCAHSHHPSLDDIGCTDLHENLGVVWVFK 900
DB 841 PIGRCGEPRNRCAPHFENWPDLCSCRDGKCAHSHHPSLDDIGCTDLHENLGVVWVFK 900
QY 901 IKTOEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLOLETKEVYTEAKEAVDA 960
DB 901 IKTOEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLOLETKEVYTEAKEAVDA 960
QY 961 LFDVDSQYNRLQADTNGIMTHAADKLVHRIREAYLSLSVPGVNAEIPBELEGRIITAIS 1020
DB 961 LFDVDSQYNRLQADTNGIMTHAADKLVHRIREAYLSLSVPGVNAEIPBELEGRIITAIS 1020
QY 1021 LDYARNVKNQDFNNGLACWNVKGVHDVQSHHRSVLVPIPEWAEVSQAVRVCPCRGYIL 1080
DB 1021 LDYARNVKNQDFNNGLACWNVKGVHDVQSHHRSVLVPIPEWAEVSQAVRVCPCRGYIL 1080
QY 1081 RVTAYKEGEGECVTHIEENNTDELKPKNCEEEVYPTDCTCNDYTAHQGTAVCNERN 1140
DB 1081 RVTAYKEGEGECVTHIEENNTDELKPKNCEEEVYPTDCTCNDYTAHQGTAVCNERN 1140
QY 1141 AGYEDAYEVDTTASVNYKPTVEEYTVDRDNHCEYDRGVYVNPPLPAGYVTKBLEYFP 1200
DB 1141 AGYEDAYEVDTTASVNYKPTVEEYTVDRDNHCEYDRGVYVNPPLPAGYVTKBLEYFP 1200
QY 1201 ETDKWIEIGETEGKFIVDSVLLMEE 1228
DB 1201 ETDKWIEIGETEGKFIVDSVLLMEE 1228

RESULT 3
US-10-428-961-63
; Sequence 63, Application US/10428961
; Publication NO. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupa, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 1227
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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-428-961-63
Query Match 91.3%; Score 5912.5; DB 14; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1127; Conservative 36; Mismatches 62; Indels 5; Gaps 3;
QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
DB 1 LTSNRKNEIINALSIPAVSNHSAQMLSDARIEDSLCIAEGNNIDPFVSASTVQTGI 60
QY 61 NIAGRILGVLPFAGQIASFYSPLVGLWPRGRDQWEIFLEHVBQLINQOITENARNTA 120
DB 61 NIAGRILGVLPFAGQIASFYSPLVGLWPRGRDQWEIFLEHVBQLINQOITENARNTA 120
QY 121 LARLOGLGDSFRAYQOOSLEDWLENRDDARTSVLTQVIALELDLFINAMPLFAIRNOEVP 180
DB 121 LARLOGLGDSFRAYQOOSLEDWLENRDDARTSVLTQVIALELDLFINAMPLFAIRNOEVP 180
QY 181 LLWVYQAANLHLLLRDASLFGSEFGLTSQEIORYYEROVBOTRDYSDYCVWYNTGLN 240
DB 181 LLWVYQAANLHLLLRDASLFGSEFGLTSQEIORYYEROVBOTRDYSDYCVWYNTGLN 240
QY 241 SLRGTAASVWRYNQFRDLTLGVLDLVALFPYSYDTRTYPIINTSAQLTREYVTDAGTG 300
DB 241 SLRGTAASVWRYNQFRDLTLGVLDLVALFPYSYDTRTYPIINTSAQLTREYVTDAGTG 300
QY 301 V--NWASWVWNNNAPSPSAIETAVIRSPHLLDFLEQTIFSTSSRWASRMTWYRGHT 358
DB 301 APSGFASTWNNNAPSPSAIETAVIRSPHLLDFLEQTIFSTSSRWASRMTWYRGHT 358
QY 359 IQSRPIGGLTSTHGNTNTSINPVLSPFSDRVVWTSYAGVLLGWVLEPIHGVPVTR 418
DB 359 IQSRPIGGLTSTHGNTNTSINPVLSPFSDRVVWTSYAGVLLGWVLEPIHGVPVTR 418
QY 419 FNRNPONTFERGTANYSQYESPGQLQKQDSELPPTTERPNYTESYSHRLSHGLISQ 478
DB 419 FNRNPONTFERGTANYSQYESPGQLQKQDSELPPTTERPNYTESYSHRLSHGLISQ 478
QY 479 SRVHVYVSWTHRSADRTNTSSDSITQIPLVKSFNLSGTSVWSGPGFTGDDIIRTNVN 538
DB 479 SRVHVYVSWTHRSADRTNTSSDSITQIPLVKSFNLSGTSVWSGPGFTGDDIIRTNVN 538
QY 539 GSVLSMGLNFNTSLQRYRVRVYAAASQTMVLRVTVGSTTFDQGFPTMSANESLTSQS 598
DB 539 GSVLSMGLNFNTSLQRYRVRVYAAASQTMVLRVTVGSTTFDQGFPTMSANESLTSQS 598
QY 599 FRPAEFPVGISASGSGTAGISINNAGROTTHFKIEPIPTATFEAYDIERAQEAVNA 658
DB 599 FRPAEFPVGISASGSGTAGISINNAGROTTHFKIEPIPTATFEAYDIERAQEAVNA 658
QY 659 LFTNTNPRRLKTDVTDYHIDOVSNLVACLDEFCLDEKRELLEKVKYAKRLSDERNLLQD 718
DB 659 LFTNTNPRRLKTDVTDYHIDOVSNLVACLDEFCLDEKRELLEKVKYAKRLSDERNLLQD 718
QY 719 PNFTSINKQPDFISTNEQSNFTSIHQSEHGWGSENIITQEGNDVFKENYVTLPGTFNE 778
DB 719 PNFTSINKQPDFISTNEQSNFTSIHQSEHGWGSENIITQEGNDVFKENYVTLPGTFNE 778
QY 779 CYPTLYQKIGESLSEKATRYQLRGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWPLSV 838
DB 779 CYPTLYQKIGESLSEKATRYQLRGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWPLSV 838
QY 839 ESPIGRCGEPRNRCAPHFENWPDLCSCRDGKCAHSHHPSLDDIGCTDLHENLGVVWV 898
DB 839 ESPIGRCGEPRNRCAPHFENWPDLCSCRDGKCAHSHHPSLDDIGCTDLHENLGVVWV 898
QY 899 FKIKTOEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLOLETKEVYTEAKEAV 958
DB 899 FKIKTOEGHARLGNLEFIEEKPLLGEALSRVKRAEKKWRDKREKLOLETKEVYTEAKEAV 958
QY 959 DALFVDSQYNRLQADTNGIMTHAADKLVHRIREAYLSLSVPGVNAEIPBELEGRIITA 1018
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Db 958 DALFVDSQYDLQADTTIGMIHAADKLVRIRREAYLSLSVPGVNAEIFEELEGRITTA 1017
Qy 1019 ISLYDARNVVKNGDFNNGLACWNVKGVHDVQOQSHRSVLVPEWEAEVSOAVRVCGRGY 1078
Db 1018 ISLYDARNVVKNGDFNNGLACWNVKGVHDVQOQSHRSVLVPEWEAEVSOAVRVCGRGY 1077
Qy 1079 ILRTAYKEGVEGCVTHIEIENNTDELKPKNCBEEVYPTDTGTCDNYTAHQGTAVCNS 1138
Db 1078 ILRTAYKEGVEGCVTHIEIENNTDELKPKNCBEEVYPTDTGTCDNYTAHQGTAVCNS 1137
Qy 1139 RNAGYEDAYEVDTTASVNYKPTVEEYTTDVRDNHCEYDRGVVNYPPPLPAGYMTKELEY 1198
Db 1138 RNAGYEDAYEVDTTASVNYKPTVEEYTTDVRDNHCEYDRGVVNYPPPLPAGYMTKELEY 1197
Qy 1199 FPETDKWIEBIGETEGKPIVDSVELLMEE 1228
Db 1198 FPETDKWIEBIGETEGKPIVDSVELLMEE 1227

RESULT 4
US-10-809-953-10
; Sequence 10, Application US/10809953
; Publication No. US20040181825A1
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTI
; FILE REFERENCE: 021565-078
; CURRENT APPLICATION NUMBER: US/10/809,953
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/09/561,016
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/EP90/00905
; PRIOR FILING DATE: 1990-05-30
; PRIOR APPLICATION NUMBER: GB 89401499.2
; PRIOR FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1228
; TYPE: PRK
; ORGANISM: Bacillus thuringiensis
US-10-809-953-10

Query Match 88.6%; Score 5742; DB 16; Length 1228;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1098; Conservative 35; Mismatches 90; Indels 10; Gaps 3;

Qy 1 LTSRKNEIETINALSPVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db 1 LTSRKNEIETIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55
Qy 61 NIAGRIILGVLPVGPAGQIASFSLVCELWPRGDQWEIPLHVEQIINQOITENARNTA 120
Db 56 NIAGRIILGVLPVGPAGQIASFSLVCELWPRGDQWEIPLHVEQIINQOITENARNTA 115
Qy 121 LARIQGLGDSFRAYQQSLEDWLENRDARTSRVLTQYIALEDLDFLNAFLPAIRNOEVP 180
Db 116 LARIQGLGDSFRAYQQSLEDWLENRDARTSRVLTQYIALEDLDFLNAFLPAIRNOEVP 175
Qy 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVETRDSYCYVWYNTGLN 240
Db 176 LLMVYAAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVETRDSYCYVWYNTGLN 235
Qy 241 SLRGTNAASVRYNQFRRLTLGLVDLVALFPSYDTRTPINTSAQLTRVYTDAGTG 300
Db 236 SLRGTNAASVRYNQFRRLTLGLVDLVALFPSYDTRTPINTSAQLTRVYTDAGTG 295
Qy 301 VNMASMNWYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTYWRGHTIQ 360
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Db 296 VNMASMNWYNNAPSFSAIETAVIRSPHLLDFLEQLTIFSAKRSWNTRHMTYWRGHTIQ 355
Qy 361 SRPIGGGLNTSTHGTSNTSINPVLSPFSRDVVTWTSYAGVLLWGIYLEPIHGVPVTRFN 420
Db 356 SRPIGGGLNTSTHGATNTSINPVLSPASRDVTRTSYAGVLLWGIYLEPIHGVPVTRFN 415
Qy 421 FRNPONTFERGTANYSPYSPGLQKQDSELTPEPTTERPNYESYSHRLSHLGLISQSR 480
Db 416 FTNPQISDRGTANYSPYSPGLQKQDSELTPEPTTERPNYESYSHRLSHLGLISQSR 475
Qy 481 VHVSVSWTHRSADRTNTISSDSITOIPLVKSPFNASGTSVWSPGPTGCDIIRTNWGS 540
Db 476 VNVVYSWTHRSADRTNTIGPNRITQIPMWKASELPQGTTVVRGPGPTGCDILRRNTGCG 535
Qy 541 VLSMGLNFNNTSLQRYVRVRYAASQTMVLRVTVGGSTTFDQGFPSPTANESLTSQSPR 600
Db 536 FGPVRTVNGPLTQRYRIGFRYASTVDFDFFVSRGGTTVNNFRFLRTMNSGDELKYGNFV 595
Qy 601 FAEPFPGVIGSAGSQ-TAGISISNNAGROTFHFDKIEFIPITATFPAEYDLERAQAVNAL 659
Db 596 RRAFTTPTFTQIIDIIRTSIOGLSNGEVYIDKIEIIPVTATFPAEYDLERAQAVNAL 655
Qy 660 FTWNPRLKTDVTDYHIDQVSNLVACLSDFCLEKRELLKVKYAKRLSDERNLQDP 719
Db 656 FTWNPRLKTDVTDYHIDQVSNLVACLSDFCLEKRELLKVKYAKRLSDERNLQDP 715
Qy 720 NFTSINKQDPDSTNEQSNFTSIHQSEHGWSNITIQEGNDVFKENYVTLPGTFNEC 779
Db 716 NFTSINKQDPDSTNEQSNFTSIHQSEHGWSNITIQEGNDVFKENYVTLPGTFNEC 775
Qy 780 YPTLYQKIGESSELKAYTRYQLRGYIEDSQDLLEIYLRYNKAKHETLDVPGTESWPLSVE 839
Db 776 YPTLYQKIGESSELKAYTRYQLRGYIEDSQDLLEIYLRYNKAKHETLDVPGTESWPLSVE 835
Qy 840 SPIGRGCEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFSLDIDIGCTDLHENLGVWVVF 899
Db 836 SPIGRGCEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFSLDIDIGCTDLHENLGVWVVF 895
Qy 900 KIKTOEGHARLGNLEFIEEKLPLGEALSVRKAKKWRDKREKLOLETKRYVTEAKEVD 959
Db 896 KIKTOEGHARLGNLEFIEEKLPLGEALSVRKAKKWRDKREKLOLETKRYVTEAKEVD 955
Qy 960 ALFVDSQYDLQADTTIGMIHAADKLVRIRREAYLSLSVPGVNAEIFEELEGRITTA 1019
Db 956 ALFVDSQYDLQADTTIGMIHAADKLVRIRREAYLSLSVPGVNAEIFEELEGRITTA 1015
Qy 1020 SLYDARNVVKNGDFNNGLACWNVKGVHDVQOQSHRSVLVPEWEAEVSOAVRVCGRGY 1079
Db 1016 SLYDARNVVKNGDFNNGLTWNVKGHDVQOQSHRSVLVPEWEAEVSOAVRVCGRGY 1075
Qy 1080 LRVTAYKEGVEGCVTHIEIENNTDELKPKNCBEEVYPTDTGTCDNYTAHQGTATA 1135
Db 1076 LRVTAYKEGVEGCVTHIEIENNTDELKPKNCBEEVYPTDTGTCDNYTAHQGTACADA 1135
Qy 1136 CNSNAGYEDAYEVDTTASVNYKPTVEEYTTDVRDNHCEYDRGVVNYPPPLPAGYMTKE 1195
Db 1136 CNSNAGYEDAYEVDTTASVNYKPTVEEYTTDVRDNHCEYDRGVVNYPPPLPAGYMTKE 1195
Qy 1196 LEYPPETDKWIEBIGETEGKPIVDSVELLMEE 1228
Db 1196 LEYPPETDKWIEBIGETEGKPIVDSVELLMEE 1228
```

```
RESULT 5
US-09-988-462-7
; Sequence 7, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Deesai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
```



```
/ TELEFAX: 512/474-7577
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1189 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-972-175-59

Query Match          54.1%; Score 3502.5; DB 10; Length 1189;
Best Local Similarity 57.0%; Pred. No. 1.6e-262;
Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps 20;

QY 7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
DB 5 NQNCIPYCLSS-----NPEVLIDGERISTGN-----SSDISLSLVQ 43

QY 65 RILGVLGVPPAGQIASFYSLVGLWPRGROQWEIHFLEHVEQLINQITENARNPTALARL 124
DB 44 FLVSNP-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

QY 125 QGLGDSFRAYQOSLEDWLENRDDARTSVLYTYQYIALELDPLNAPLFAIRNOEVPILMV 184
DB 100 EGLGNFNIIYEAFAKEWEEDPNPATRTRVIDRFRILDGLLERDIPSPFAISGFEVPLLSV 159

QY 185 YAAQANLHLLLRDASLFGSBEFLTSQEIORYYERQVEQTRDYSYCVWYNTGLNSLRG 244
DB 160 YAAQANLHLLLRDASLFGSBEFLTSQEIORYYERQVEQTRDYSYCVWYNTGLNSLRG 244

QY 245 TNAASWRYNQPRDLTLGLVDLVALFPSTYRTYPTINTSAQLTREVTYDAIGATGVNMA 304
DB 220 STYQDWITVYRRLRLDLTLVLDIAAFFPNYDNRYPYIQPVGQLTREVTYDPL---INFN 275

QY 305 SMTWNNAPPSALETAVIRSPHLLDFLEQLTIFSTSRWSATHMYWRGHTTQSRPI 364
DB 276 POLQSAVQAQPTFNVMSSAIRNPHLFDILNLTIFTD---WFSVGRNFGWGHRRVISSLI 332

QY 365 GGLNTSTHGSTNTSINPRLSPFSDRVVWTSYAGVLL---WGIYLEPIHGVTFRFN 420
DB 333 GCGNTSTIYGREANQBPSTFGPVFTLSNPTLRLLOQPWAPPFNLRGVBGVFS 392

QY 421 FRNPQTFE---RGTYANSQPYSPGLQKDSBELPPTETPRPNYESYSHRLSHIGLIS 477
DB 393 --TPTNSFTYRGRTV-----DSLTLPEDNSVPPREGYSRHLCHATFVQ 436

QY 478 QSRVHV-----PVYSWTHRSADRTNISDSITQIPLVKSFNLSGTSVVSQPGFTGGDI 533
DB 437 RSGTFLPTGTVVFSWTHRSATLTNTIDPERINQIPLVGRFVWVGTSVITGPGFTGGDI 496

QY 534 RTNVNGLSVLSMGLNFNNTSLQRYRVRVYAAQO-----TMVLRTVTVGGSTTRDQGPFS 586
DB 497 RNTTGDVFSVQVNNINSITQRYLRFRYASRRDARVIVLTGAAGTGGVGGQVSNMPLQK 556

QY 587 TMSANESITQSFRFAEPP-----VGISAGSQTAGISISNAGRQTTFHFKIE 635
DB 557 TWEIGENLTSRTFRYTDFSNPPSPRANPDIIIGISEQLPFGAG-SISSG---ELYDKIE 611

QY 636 FIPITATEAEYDLERAQEVNALTNTNPRRLKTDVTDYHIDQVSNLVACLSDBFCLDE 695
DB 612 IILADATTAEASDLERAQKAVNALFTSSNQGLKTDVTDYHIDQVSNLVCLSDBFCLDE 671

QY 696 KRELLEKVKYAKRLDERMLQDPNFTSINKQPDFISTNEQSNTFSIHEQSEHGHWGSEN 755
DB 672 KRELSEKVKYAKRLDERMLQDPNFRGINRQPD-----RGRWGSTD 713

QY 756 ITIQGNDFVKNYYTLPGTFNECYPTLYYQKIGESLKYATRYQLRGYIEDSQLEIYL 815
DB 714 ITIQGDDVFKENYYTLPGTVDCEYPTLYYQKIDESLKYATRYELRGYIEDSQLEIYL 773

QY 816 IRYNAKHETLDVPGTESWPLSVESPIGRGCEPNRCAPHFENPNPDLDCSRDGEKCAHHS 875
DB 774 IRYNAKHETLDVPGTESWPLSVESPIGRGCEPNRCAPHFENPNPDLDCSRDGEKCAHHS 833
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QY 876 HHFSLDIDIGCTDLHENLGWVVPFKIKTOEGHARLGNLEFIEBEKPLLGALSRVRAEKK 935
DB 834 HHFTLDDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFIEBEKPLLGALSRVRAEKK 893

QY 936 WRDKREKLOLETQRYVYTEAKAVDALFYDSQYNRLQADTNGIMHAADKLVRHIREAYLS 995
DB 894 WRDKREKLOLETQRYVYTEAKAVDALFYDSQYNRLQADTNGIMHAADKLVRHIREAYLP 953

QY 996 ELSVTIPGVNAIEFELEGRIITATSLYDARNVVKNGDFNGLACVNVKGVHDV-QQSHHR 1054
DB 954 ELSVTIPGVNAIAFELEGRIIFTAYSLYDARNVVKNGDFNGLACVNVKGVHDVBSQNNHR 1013

QY 1055 SVLVTIPEAEVSOAVRVCPCRGYILRTVYAKYGGEGCVTIHEENTNTDELKFNCEBE 1114
DB 1014 SVLVTIPEAEVSOAVRVCPCRGYILRTVYAKYGGEGCVTIHEENTNTDELKFNCEBE 1073

QY 1115 EYVPDTCTCNDYTA---HOGTAVCNSRNAGYEDAYEVDVTTASVNYKPTYEEETVDVR 1170
DB 1074 EYVPNTVTCCNYTGTQBEYEGT--YTSRNQGYDEAYGNPNPSPADYASVYEEKSYTDGR 1131

QY 1171 RDNCEYDRGVYVPPPLPAGYMTKLEYFPETDKWIRIGETEGKFIYDSVVELLMEE 1228
DB 1132 RENPCESNRGYGDTPLPAGYMTKLEYFPETDKWIRIGETEGKFIYDSVVELLMEE 1189

RESULT 8
US-10-200-522-59
; Sequence 59, Application US/10200522
; Publication No. US20030195336A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Mettus, Anne Marie Light
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-1
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: MECO:213 (11792.0213 DVUS01)
; CURRENT APPLICATION NUMBER: US/10/200,522
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/337,280
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 08/980,071
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 08/757,536
; PRIOR FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent in version 3.1
; SEQ ID NO. 59
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Delta Endotoxin
US-10-200-522-59

Query Match          54.1%; Score 3502.5; DB 14; Length 1189;
Best Local Similarity 57.0%; Pred. No. 1.6e-262;
Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps 20;

QY 7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
DB 5 NQNCIPYCLSS-----NPEVLIDGERISTGN-----SSDISLSLVQ 43

QY 65 RILGVLGVPPAGQIASFYSLVGLWPRGROQWEIHFLEHVEQLINQITENARNPTALARL 124
DB 44 FLVSNP-VPGGGFLVGLIDFVWGIVGP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

QY 125 QGLGDSFRAYQOSLEDWLENRDDARTSVLYTYQYIALELDPLNAPLFAIRNOEVPILMV 184
DB 100 EGLGNFNIIYEAFAKEWEEDPNPATRTRVIDRFRILDGLLERDIPSPFAISGFEVPLLSV 159

QY 185 YAAQANLHLLLRDASLFGSBEFLTSQEIORYYERQVEQTRDYSYCVWYNTGLNSLRG 244
DB 160 YAAQANLHLLLRDASLFGSBEFLTSQEIORYYERQVEQTRDYSYCVWYNTGLNSLRG 244
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Db 557 TMEIGNLRSFRYTRDFNSPFSFRANPDIIIGISEQLFGAG-SISSG-----ELYDKIE 611
Qy 636 FIPITATFAEYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLDE 695
Db 612 IILADATFAESDLERAQAVNALFTSSNIQIGLTKDVTYHIDQVSNLVACLSDSEFCLDE 671
Qy 696 KRELLEKVKYAKRLSDERNLQDPNPTSINKQDPFISTWEQSNFTSIEHQSEHGWGMSN 755
Db 672 KRELSEKVKHAKRLSDERNLQDPNFRGINRQPD-----RGRGSTD 713
Qy 756 ITIQEGNDVFKENYVTLPGTFNECYPTLYOKIGSELKAYTRYQLRGYIEDSQLEIYL 815
Db 714 ITIQGGDDVFKENYVTLPGTVDECYPTLYOKIGSELKAYTRYELRGYIEDSQLEIYL 773
Qy 816 IRYNAKHETLDVPGTESVNPVLSVESPIGRGCPNRCAPHFENWPDLDSCRCRGEKCAHHS 875
Db 774 IRYNAKHEIVNPGTGLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRCRGEKCAHHS 833
Qy 876 HPSIDIDIGCTDLHENLGVVWVFKIKTOEGHARLGNLEFIEEKLPLGALSRVRAEKK 935
Db 834 HHFTLIDVGCCTDLNEDLGVWVIFKIKTQDCHARLGNLEFIEEKLPLGALSRVRAEKK 893
Qy 936 WDKREKLOLEYKRVYTEAKEAVDALFVDSQYNRLOQADFNIGIHAADKLVRIRREAYLS 995
Db 894 WDKREKLOLEYNI VYKEAKESVDALFVNSQYDRLOQVDTNIAIHAADKRVHRIREAYLP 953
Qy 996 ELSVIPGVNAEIPFEELEGRIITAIISLYDARNVVGNGDFNGLACVWVKGHDV-QQSHUR 1054
Db 954 ELSVIPGVNAEIPFEELEGRIITAYSLYDARNVVGNGDFNGLACVWVKGHDVBEQNNHR 1013
Qy 1055 SVLVIPEWAEARVQAVRCPGGRGYILRVTAAYKEGEGCVTTIHEIENNTDELKFNCEBE 1114
Db 1014 SVLVIPEWAEARVQAVRCPGGRGYILRVTAAYKEGEGCVTTIHEIENNTDELKFNCEVE 1073
Qy 1115 EYVPTDTGTCDNYTA-----HOGTAVCNSENAGYDAYEVDVDTASVNYKPTIYEETTYDVR 1170
Db 1074 EYVPPNVTVCNNTYTQEEYEGT--YTSRNOGYDEAYGNPNVPADYASVYBEKSYTDGR 1131
Qy 1171 RDNHCYDRGYVNPPLPAGYVTKLEYPPETDKWIEIGETGKPFIVDSVELLIMEE 1228
Db 1132 RENPCSENRYGVDYPLPAGYVTKLEYPPETDKWIEIGETGKPFIVDSVELLIMEE 1189

RESULT 10
US-09-972-175-2
; Sequence 2, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MRCO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-972-175-2

Query Match 54.0%; Score 3500.5; DB 10; Length 1189;
Best Local Similarity 57.0%; Pred. No. 2.4e-262;
Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps 20;
Qy 7 NENEII--NALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAG 64
Db 5 NONQIPNCLIS-----NPBEVLDDGERISTGN-----SSIDISLVQ 43
Qy 65 RILGVLGVFPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARL 124
Db 44 FLVSNF-VPGGGFLGLIDFVWGIVP---SQMDAFLVQIEQLINERAEFARNAIANL 99
Qy 125 QGLGDSFRAYQOQSLDLENRDDARTSVLYTYQYIALBELDFLNAMPLFAIRNQEVPLLMV 184
Db 100 EGLGNFNIVYAEAFKEWEDPNPATRTRVIDRFRILDGILLERDIPSAISGEFVPLLSV 159
Qy 185 YQAQANLHLALLRDASLFGSSEGLTSQEIQRVYERQVEQTRDYSQYCVWNTYGLNSLRG 244
Db 160 YQAQANLHLALLRDSVIFGERWGLTINVENYNNLRIRHIDYADHCANTYRGLNLPK 219
Qy 245 TNAASWRYNPOFRRLDLGLVDLVALPSPYDTRTYPINTSAQLTREVYTDATGATGVNMA 304
Db 220 STYQDMITYNLRDLTLTLVDIAFFNYDNRRYPQIPVGQLTREVYTDPL-----INFN 275
Qy 305 SMNYYNNNAFSAIETAVIRSPHLLDPLEQLTIPSTSRWSATRMTYWRGHTTOSRPI 364
Db 276 PQLOSVAQLPTFNVMESAIARNPHLFDILNLTIFTD---WFSVGRNFYWGHRVSSLI 332
Qy 365 GGLGNTSTHGSTNTSINVRLSFTSRDYYWTESYAGVLL-----WGIYLEPHGVTVRN 420
Db 333 GGGNITSPYIGREANQEPFRSFTFNGPVFRLSNPTLRLLOQPWAPPFNLRGVEGVEFS 392
Qy 421 FRNPONTEP---RGTYANSQPYESPGLQLKDSLETLPETTERPNYESYSHRLSHIGLIS 477
Db 393 --TPNSFTYRGRGV-----DSLTELPEEDNSVPPREGYSHRLCHATPVQ 436
Qy 478 QSRVHV-----PVYSWTHRSADRTNTISSDSITQIPLVKSNLNGSTSVVSGPGFTGGDI 533
Db 437 RSGTPEFLTGTGVVFSWTHRSATLTNTIDPERINQIPLVKGFVWGTSTVITGEGTGGDIL 496
Qy 534 RTNVNGSVLSMGLNPNNTSLQRYRVRYAASQ-----TWLVRTVGGSTTTPDQGPFS 586
Db 497 RRTFGDFVSLQVNVINSPIQYRLRFYASRDRARIVLGTAASTGVGGQVSVNMPLOK 556
Qy 587 TWSANESLTSQSFRAEPP-----VGISASGSQTAGISISNAGRQTFHFDKIE 635
Db 557 TMEIGENLTSFTFYTDPSNPFSFRANPDIIIGISEQLFGAG-SISSG-----ELYDKIE 611
Qy 636 FIPITATFAEYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLDE 695
Db 612 IILADATFAESDLERAQAVNALFTSSNIQIGLTKDVTYHIDQVSNLVACLSDSEFCLDE 671
Qy 696 KRELLEKVKYAKRLSDERNLQDPNPTSINKQDPFISTWEQSNFTSIEHQSEHGWGMSN 755
Db 672 KRELSEKVKHAKRLSDERNLQDPNFRGINRQPD-----RGRGSTD 713
Qy 756 ITIQEGNDVFKENYVTLPGTFNECYPTLYOKIGSELKAYTRYQLRGYIEDSQLEIYL 815

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Db 714 ITIQGDDVFKENYVTLPGTVDECPYLYQKIDESKLAITYRUELRGYIEDSQDLEIYL 773
QY 816 IRYNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHFENWPDLDSCSDRGEKCAHHS 875
Db 774 IRYNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHFENWPDLDSCSDRGEKCAHHS 833
QY 876 HHFSLDIDIGCTDLHENLGVVWVFKITQEGHARLGNLFIEBEKPLLGALSRVRAEKK 935
Db 834 HHFTLDIDVGCTDLNEDLGWVIFKJKTQGHARLGNLFIEBEKPLLGALSRVRAEKK 893
QY 936 WRDKREKLOLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIIHAADKLVRHREAYLS 995
Db 894 WRDKREKLOLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIIHAADKLVRHREAYLS 953
QY 996 ELSVIPGVNAEIPFEELEGRITAIISLYDARNVKNVGNDFNGLACWNVKGVHDV-QQSHR 1054
Db 954 ELSVIPGVNAEIPFEELEGRITAIISLYDARNVKNVGNDFNGLACWNVKGVHDV-QQSHR 1013
QY 1055 SVLVIPWEAEVSAVRVCPGRGYILRVYAYKEGYEGGCVTHIENNTDELKPKNCCEE 1114
Db 1014 SVLVIPWEAEVSAVRVCPGRGYILRVYAYKEGYEGGCVTHIENNTDELKPKNCCEE 1073
QY 1115 EYVPTDGTGNDYTA---HQTAVCNERNAGYEDAYEDVDTTASVNYKYETTYDVR 1170
Db 1074 EYVPTDGTGNDYTA---HQTAVCNERNAGYEDAYEDVDTTASVNYKYETTYDVR 1131
QY 1171 RDNHCEYDRGVVNYPPPLPAGYVTKLEYFPETDKVWIEIGETEGFIVDSVELLMEE 1228
Db 1132 RDNHCEYDRGVVNYPPPLPAGYVTKLEYFPETDKVWIEIGETEGFIVDSVELLMEE 1189

RESULT 11
US-10-200-522-2
; Sequence 2, Application US/10200522
; Publication No. US20030195336A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Mettus, Anne Marie Light
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE COMPOSITIONS ENCODING LEPIDOPTERAN-T
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: MECO:213 (11792,0213 DVUS01)
; CURRENT APPLICATION NUMBER: US/10/200,522
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/337,280
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 08/980,071
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 08/757,536
; PRIOR FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Delta Endotoxin

US-10-200-522-2

Query Match 54.0%; Score 3500.5; DB 14; Length 1189;
Best Local Similarity 57.0%; Pred. No. 2,4e-262;
Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps 20;

QY 7 NENEII--NALSPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVASASTVQTGINTAG 64
Db 5 NQNCIPYNCLSD-----NPVEVLIDGERISTGN-----SSIDISLSLVQ 43
QY 65 RIILGVGLVPPAGIAGFYSFLVGELWPRGDOWEIEFLEHVEOLINCOITENARNATLARL 124
Db 44 FLVSNF-VPGGGLVGLIDFVGVGP---SQMDAFLVQIEQLINERTAEAFARNAAIANL 99

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QY 125 QGLGDSFRAYQOQSLDMLNRRDDARTSRVLYTOYIALLELDLNPMLPFAIRNQVPLIMV 184
Db 100 EGLGNFNFIYVEAFKEWEEPPNPATRTVRIDFRILDDGLLERDIPSFALSGEVPPLSV 159
QY 185 YAOAANLHLLLRDASLFGSEFGLTSQEIQRYTERQVEQTRDYSDYCVWVNTGLNSLRG 244
Db 160 YAOAANLHLLLRDASLFGSEFGLTSQEIQRYTERQVEQTRDYSDYCVWVNTGLNSLRG 219
QY 245 TNAASWVRVYNOQRDLTLGVLDLVALPSPYDTRTYPTINTSAQLTRREYTDIAGATVMA 304
Db 220 STYQDWITYNRLRRDLTLVLDIAAFPPYDNRYPYPIQPVGQLTRREYTDPL----INFN 275
QY 305 SMWYNNNAPSFAETAIVIRSPHLLDLEQLTIFSTSSRSWASATRHMTYWRGHTIOSRPI 364
Db 276 PQLQSVQAQLPTFNWMESSAIRNPHLPDILNLTFTD---WPSVGRNFWGHRVLSLI 332
QY 365 GGGINTSTHGSTWTSINPRLSFFSRDQVWTESYAGVLL---WGYLEBPIHGVPVTRFN 420
Db 333 GGGNITSPIYGRANOEPPRSFTFNGPVFRTLSNPTLRLLQQPWPAPPNLRGVEGVETS 392
QY 421 FRNPONTFE---RGTYANSQPYESPGLQKDSLETLPPTETTERPNYESYSHRSLHGLIS 477
Db 393 --TPTNSFTVRGRGTV-----DSLETLPEDNSVPPREGYSHRLCHATFVQ 436
QY 478 QSRVHV----PYVSWTHRSADRTNTISSDITQIPLVKSFNLSNGTSVSVSGFTGGDI 533
Db 437 RSGTFLTTGTVFVSWTHRSATLNTIDPERINQIPLVKGFRVWGTSVITPGFTGGDIL 496
QY 534 RTNVNGLSVMLGNFNTSLQRYVRVRYAASQ-----TWVLRVTVGGSTTFPOGPPS 586
Db 497 RNTFGDFVSLQVNLNSPITQYRURFYASRDRARVILVTGAASTGVGGQSVNMLPQK 556
QY 587 TMSANESLTSQSFRAEFP-----VGISAGSQTAGISISNNAAGRTFHFDKIE 635
Db 557 TMEIGENLTSRTFRYTFDFSNPFRANPDIIIGISQPLFGAG-SISGG----ELYDKIE 611
QY 636 FPIPTATPEAVDLERAQEAVALFTNTNPRRLKTDVTDYHDIDQVSNLVLACDSDFCLDE 695
Db 612 ILADATPEASDLERAQEAVALFTNTNPRRLKTDVTDYHDIDQVSNLVLACDSDFCLDE 671
QY 696 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPPFI STNEQSNFTS IHEQSEHGWGSEN 755
Db 672 KRELSEKVKHAKRLSDERNLLQDPNFRGINQPD-----RHRGSTD 713
QY 756 ITIQGDDVFKENYVTLPGTVDECPYLYQKIDESKLAITYRUELRGYIEDSQDLEIYL 815
Db 714 ITIQGDDVFKENYVTLPGTVDECPYLYQKIDESKLAITYRUELRGYIEDSQDLEIYL 773
QY 816 IRYNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHFENWPDLDSCSDRGEKCAHHS 875
Db 774 IRYNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHFENWPDLDSCSDRGEKCAHHS 833
QY 876 HHFSLDIDIGCTDLHENLGVVWVFKITQEGHARLGNLFIEBEKPLLGALSRVRAEKK 935
Db 834 HHFTLDIDVGCTDLNEDLGWVIFKJKTQGHARLGNLFIEBEKPLLGALSRVRAEKK 893
QY 936 WRDKREKLOLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIIHAADKLVRHREAYLS 995
Db 894 WRDKREKLOLETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMIIHAADKLVRHREAYLS 953
QY 996 ELSVIPGVNAEIPFEELEGRITAIISLYDARNVKNVGNDFNGLACWNVKGVHDV-QQSHR 1054
Db 954 ELSVIPGVNAEIPFEELEGRITAIISLYDARNVKNVGNDFNGLACWNVKGVHDV-QQSHR 1013
QY 1055 SVLVIPWEAEVSAVRVCPGRGYILRVYAYKEGYEGGCVTHIENNTDELKPKNCCEE 1114
Db 1014 SVLVIPWEAEVSAVRVCPGRGYILRVYAYKEGYEGGCVTHIENNTDELKPKNCCEE 1073
QY 1115 EYVPTDGTGNDYTA---HQTAVCNERNAGYEDAYEDVDTTASVNYKYETTYDVR 1170
Db 1074 EYVPTDGTGNDYTA---HQTAVCNERNAGYEDAYEDVDTTASVNYKYETTYDVR 1131
QY 1171 RDNHCEYDRGVVNYPPPLPAGYVTKLEYFPETDKVWIEIGETEGFIVDSVELLMEE 1228

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Db 1132 RENPCENRGYDTPPLPAGYTKOLEYFETDKWIEIGETEGTIVDSVLELLMEE 1189

RESULT 12

US-10-855-535-2

Sequence 2, Application US/10855535

Publication No. US20040221334A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Gilmer, Amy Jelen

APPLICANT: Mettuss, Anne-Marie Light

TITLE OF INVENTION: Antibodies Immunoreactive with Lepidopteran-Toxic Polypeptides

TITLE OF INVENTION: and Methods of Use (Amended)

FILE REFERENCE: 11792.0214.DVUS02

CURRENT APPLICATION NUMBER: US/10/855,535

CURRENT FILING DATE: 2004-05-27

PRIOR APPLICATION NUMBER: 09/337,635

PRIOR FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: 08/980,071

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: 08/757,536

PRIOR FILING DATE: 1996-11-27

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patent in version 3.2

SEQ ID NO 2

LENGTH: 1189

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Recombinant Delta Endotoxin

US-10-855-535-2

Query Match 54.0%; Score 3500.5; DB 17; Length 1189;

Best Local Similarity 57.0%; Pred. No. 2.4e-262; Matches 109; Gaps 20;

Matches 717; Conservative 143; Mismatches 289; Indels 109; Gaps 20;

QY 7 NENEII--NALSIPAVSNHSTQMDLSIPARIBDSLCIAEGNNINPLVBSASTVQTGINIAG 64

Db 5 NQNCIPYNCLS-----NPEVLLDGERISTGN-----SSIDISLSLVQ 43

QY 65 RILGVLGVPPAGQIAFSFVLGELWPGRDQWEI FLEHVEQLINQQTENANNTALRL 124

Db 44 FLVSNF-VPGGFLVGLIDFVGVIGVP---SQWDAFLVQIEQLINERIAEFARNAAIANL 99

QY 125 QSLGDSERAYQCSLEMDLENRDDATRSVLYTQYIALELDPLNAPLEAIRNQEVPLMV 184

Db 100 EGLGNFNIIYAFKWEEDPNPNATRTVDIFRLDGLLERDIPSPAISGFEVPLLSV 159

QY 185 YAAANLHLLLRDASLFGSEGLTSQEIQRYYERQVQTRDYSQYCVWNTGLNSLRG 244

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Db 220 STYQDWITYNRLRLDLTLVLDIAAFFNNDNRYPQIPVGQLTREVYTDPL----INFN 275

QY 305 SNNYNNNAPSALETAVIRSPHLLDLEQLTIFSTSSRSATRHMTYWRGHTIQSRPI 364

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QY 365 GGGLNTSTHGSTNTINPVRLSFFSRDQVWVWTSYAGVLL---WGYLEPIHGVTVRFN 420

Db 333 GGGNITSPYIGREANQEPSPSTFNGPVFRTLSNPTLRLQQPWAPPNLRGVEGVFS 392

QY 421 FRNPQWTE---RGYANSQPYESGLQLKQSETELPPETTERPNYSYHRLSHIGLIS 477

Db 393 --TPTNSFTYRGRTV-----DSLTELPPEDNSVPREGYSHRLCHATFVQ 436

QY 478 QSRHVH----PVYSWHRSADTNTIISDSTIQIPLVKSFLNLSGTSVVSQPGTGGDI 533

Db 437 RSGTFLTTGVVFSWTHRSATLNTIDPERINQIPLVRGFRVWGTSVITGPGTGGDIL 496

QY 534 RTNVNGSVLSMGLNFNNTSLQRYVRVRYAASQ-----TMVLRVTVGSTTFQGFPS 586

Db 497 RENTFGDFVSLQVNLINSPIITQRYRLRFRYASSRDARVILTGAASTGVGGQVSNMPLQK 556

QY 587 TMSANESLTSQSRFPABPP-----VGISASGSQTAGISISNAGRTQTFHPDKIE 635

Db 557 TMEIGENLTSTRYTFDSNPFSPFRANPDIIIGISQPLFGAG-SISSG-----ELYIDKIE 611

QY 636 FIPITATFEAEYDLERAQEAENVNALTNTNPRRLKTDVTDYHIDOVSNLVACLSDFECLDE 695

Db 612 ILLADATFEASDRLERAQVNAALFTSSNQGLKTDVTDYHIDOVSNLVACLSDFECLDE 671

QY 696 KRELLEKVKYAKRLSDERNLQDNPFTSINKQPDFISTNEQSNFTSIIHQSHGWSGSSN 755

Db 672 KRELSEKVKHAKRLSDERNLQDNPFRGINRQPD-----RGMRGSTD 713

QY 756 ITIQEGNDVFKENYVTLPGTFNECYPTLYYQKIGESLKYTRYOLRGYIEDSQLEIYL 815

Db 714 ITIQGGDDVFKENYVTLPGTFNECYPTLYYQKIDESKLKAYTRYELRGYIEDSQLEIYL 773

QY 816 IRYNAKHETLDVPGTESVPLSVESPIGRCEPNRCAPHFENWPDLDSCRCRGEKCAHHS 875

Db 774 IRYNAKHEIVNVPGTSLWPLSAQSPICGCEPNRCAPHLEWPDLDSCRCRGEKCAHHS 833

QY 876 HFSLDIDIGCTDLHENLGVWVVFVKIKTQEGHARLGNLEFIEBEKPLLGEALSVRKRAKK 935

Db 834 HHFTLIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFIEBEKPLLGEALSVRKRAKK 893

QY 936 WRDKREKLOLSTKRYVTEAKAVDALFVDSQYNRLQADTNIGMIHAADKLVRHIREAYLS 995

Db 894 WRDKREKLOLSTKRYVTEAKAVDALFVDSQYNRLQADTNIGMIHAADKLVRHIREAYLS 953

QY 996 ELSVTPGVNARI FEELEGRIITATSLYDARNVWKNNGFNGLACVNVKHGVDV-QQSHHR 1054

Db 954 ELSVTPGVNARI FEELEGRIITATSLYDARNVWKNNGFNGLACVNVKHGVDV-QQSHHR 1013

QY 1055 SVLVIPEWAEVSAQVRVCPGCGYILRVATYKEGYEGECVTIHEIENNTDELKFCNCEE 1114

Db 1014 SVLVIPEWAEVSAQVRVCPGCGYILRVATYKEGYEGECVTIHEIENNTDELKFCNCEE 1073

QY 1115 EYPTDITQTCNDYTA-----HOGTAVCNRRNAGYEDAYEVDVTASVNYKPTTBEETVTVR 1170

Db 1074 EYPTDITQTCNDYTA-----HOGTAVCNRRNAGYEDAYEVDVTASVNYKPTTBEETVTVR 1131

QY 1171 RDNHCEYDGRGVNYPPLPAGYTKOLEYFETDKWIEIGETEGTIVDSVLELLMEE 1228

Db 1132 RENPCENRGYDTPPLPAGYTKOLEYFETDKWIEIGETEGTIVDSVLELLMEE 1189

RESULT 13

US-09-972-175-61

Sequence 61, Application US/09972175

Publication No. US20030101482A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

Gilmer, Amy Jelen

Mettuss, Anne-Marie Light

TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:


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Db 393 --TPNSFTYRGRTV-----DSLTELPEEDNSVPPREGYSHRLCHATFVQ 436
Qy 478 QSRVHV-----PVYSWTHRSADRTNTISSDSITQIPLVKSPNLNSGTSVWSGPGFTGGDI 533
Db 437 RSGTFFLTGTVFVSWTHRSATLNTWIDPERINQIPLVKGFRVWGTSVITGPGFTGGDIL 496
Qy 534 RTNVNGSVLSGLNPNNTSLQRVVRVYAAO-----TMVLRVTVGSTTFDQGFPS 586
Db 497 RRTFGDFVSLQVNNINSPITQRYRLFRYASSDARVIVLTGAASTGVGGQSVNNPLQK 556
Qy 587 TMSANESLTSQSRFAEFP-----VGISASGSQTAGISISNNAGRQTFHFDKIE 635
Db 557 TMEIGENLTSRTFRYTDSPFPFRANPDIIIGISEQLFGAG-SISSG-----ELYIDKIE 611
Qy 636 PIPITATFEAYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDDEFCLDE 695
Db 612 IILADATFEABSDLEAQAQVNAFTSSNQIGLKTDTVDYHIDQVSNLVCLSDDEFCLDE 671
Qy 696 KRELLEKVKYAKLSDERNLLQDPNFTSINKOPDFTSTNEQSNFTSIHQSEHGWGSEN 755
Db 672 KRELSEKVKHAKLSDERNLLQDPNFRGINRQPD-----RGRGSTD 713
Qy 756 ITIQEGNDVFKENYVTLPGTFNECVPTLYQKIGESLKAQYQYQYQYQYQYQYQYQYQY 815
Db 714 ITIQGGDDVFKENYVTLPGTVDECVPTLYQKIDESKLKAYTRVELGYIEDSQDLEIYL 773
Qy 816 IRYNAKHETLDVPGTSVWPLSVESPIGRCGEPNRCAPHFENWPDLDSCSDGKCAHHS 875
Db 774 IRYNAGHEIVNPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSDGKCAHHS 833
Qy 876 HHFSLDIDIGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEEKPILLGEALSRVKRAEKK 935
Db 834 HHFTLIDIVGCTDLNEDLGVWVFKIKTQDGHARLGNLEFIEEKPILLGEALSRVKRAEKK 893
Qy 936 WRDKREKLETKRYVTEAKEAVDALFVDSQYNRLQADTNIGMHAADKLVHRIREAYLS 995
Db 894 WRDKREKLETKRYVTEAKEAVDALFVDSQYNRLQADTNIGMHAADKLVHRIREAYLP 953
Qy 996 ELSVTPGVNAEIFELEGRIITAIISLYDARNVKNNGFNGLACWNVKGHVQV-QQSHHR 1054
Db 954 ELSVTPGVNAEIFELEGRIITAIISLYDARNVKNNGFNGLACWNVKGHVQVVEEQNNHR 1013
Qy 1055 SVLVIPWEAEVSQAVRVCGRGYLLRTAYKEGYGEGCVTIHEIENNTDELKPKNCEE 1114
Db 1014 SVLVIPWEAEVSQAVRVCGRGYLLRTAYKEGYGEGCVTIHEIENNTDELKPKNCEE 1073
Qy 1115 EYVPTDTGTCNDYTA---HOGTAVCNRNAGYDAYEVDTTASVNYKPTYEEETVDYR 1170
Db 1074 EYVPTDTGTCNDYTA---HOGTAVCNRNAGYDAYEVDTTASVNYKPTYEEETVDYR 1131
Qy 1171 RDNHCEYDRGVNYPPLPAGYMTKELEYFPETDKWIEIGETEGKFIVDSVELLMEE 1228
Db 1132 RENCESNRGYGDTPLPAGYMTKELEYFPETDKWIEIGETEGKFIVDSVELLMEE 1189

```

Search completed: November 21, 2004, 17:04:22
Job time : 119 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2004, 16:50:34 ; Search time 43 Seconds
(without alignments)
2747.772 Million cell updates/sec

Title: US-10-614-524-2

Perfect score: 6479

Sequence: 1 LTSNRKNEIINALSIPAV.....ICETGKEFVDSVELLMEE 1228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	5745	88.7	1228	2	S00873
2	3791	58.5	1176	2	A48970
3	3484.5	53.8	1189	2	S00944
4	3433.5	53.0	1165	2	S11446
5	3433	53.0	1166	2	S32645
6	3426.5	52.9	1181	2	A41052
7	3421	52.8	1171	2	I40572
8	3413.5	52.7	1174	2	S32649
9	3412.5	52.7	1176	2	JT0241
10	3412.5	52.7	1174	2	A42459
11	3411	52.6	1160	2	S32647
12	3405.5	52.6	1176	2	JC2219
13	3400.5	52.5	1176	2	S02215
14	3399.5	52.5	1176	2	A22617
15	3399.5	52.5	1178	1	US85XH
16	3399	52.5	1171	2	A37829
17	3387	52.3	1177	2	A49785
18	3323.5	51.3	1172	2	S32689
19	3283	50.7	1155	2	JD0002
20	3269	50.5	1155	2	A25513
21	3268	50.4	1155	2	S02134
22	3257.5	50.3	1156	2	A29125
23	3251	50.2	1155	2	I39838
24	3161.5	48.8	1156	2	A29838
25	2434	37.6	934	2	A22798
26	2294.5	35.4	1138	2	A48944
27	2200.5	34.0	1157	1	S49247
28	2170.5	33.5	719	2	I40590
29	2116	32.7	719	2	I39815

30	2107	32.5	719	2	S25383	parasporal crystal
31	2101	32.4	719	2	I39814	insecticidal prote
32	2002	30.9	1160	2	I40589	parasporal crystal
33	1947.5	30.1	1154	2	S39536	parasporal crystal
34	1930	29.8	823	2	S04181	parasporal crystal
35	1621	25.0	1156	2	S19306	parasporal crystal
36	1616.5	24.9	1136	1	US8581	parasporal crystal
37	1511.5	23.3	1180	2	I39870	parasporal crystal
38	1498.5	23.1	1180	2	A26858	parasporal crystal
39	1227	18.9	380	2	B42459	hypothetical prote
40	1164	18.0	655	2	JC7140	protoxin - Bacilli
41	1064	16.4	652	2	A27323	parasporal crystal
42	1062.5	16.4	659	2	S10228	parasporal crystal
43	1053.5	16.3	652	2	I39811	parasporal crystal
44	999.5	15.4	649	1	JH0261	parasporal crystal
45	987.5	15.2	618	2	S11445	parasporal crystal

ALIGNMENTS

RESULT 1

S00873

Parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N:Alternate names: parasporal crystal protein cryA4

C:Species: Bacillus thuringiensis subsp. thuringiensis

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: S00873

R:Brizzard, B.L.; Whiteley, H.R.

Nucleic Acids Res. 16, 2723-2724, 1988

A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus

A:Reference number: S00873; MUID:88203216; PMID:3362680

A:Accession: S00873

A:Molecule type: DNA

A:Residues: 1-1228 <BRI>

A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094

C:Genetics:

A:Gene: cryA4

A:Start codon: TTG

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match	88.7%	Score 5745;	DB 2;	Length 1228;
Best Local Similarity	89.1%	Pred. No. 0;		
Matches 1098;	Conservative 35;	Mismatches 90;	Indels 10;	Gaps 3;
Qy	1	LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCTAEGNNINPLVSASTVQTGI	60	
Db	1	MTSNRKNEIIN-----AVSNHSAQMDLLPDARIEDSLCTAEGNNIDPFVSASTVQTGI	55	
Qy	61	NIAGRIILGVLPAGQIATSPYSLVGLWPRGRDQWEIFLEHVQLINQQITENARNTA	120	
Db	56	NIAGRIILGVLPAGQIATSPYSLVGLWPRGRDQWEIFLEHVQLINQQITENARNTA	115	
Qy	121	LARIQLGDSFRAYQQSLDLEWLNRRDARTSVLYTQYIALELDFLNAFLPAIRNQVEVP	180	
Db	116	LARIQLGDSFRAYQQSLDLEWLNRRDARTSVLYTQYIALELDFLNAFLPAIRNQVEVP	175	
Qy	181	LLMVAQAANLHLLLRDASLFGSEFGLTSEIORYYERQVEQTRDYSDYCVWNTGLN	240	
Db	176	LLMVAQAANLHLLLRDASLFGSEFGLTSEIORYYERQVEQTRDYSDYCVWNTGLN	235	
Qy	241	SLRGNTAASWRYNQFRDLTLGLVLDLVALPSPYDTRTPINTSAQLTRVYTTDAIGATG	300	
Db	236	SLRGNTAASWRYNQFRDLTLGLVLDLVALPSPYDTRTPINTSAQLTRVYTTDAIGATG	295	
Qy	301	VNMAWMYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRHMTYWRGHTIQ	360	
Db	296	VNMAWMYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRHMTYWRGHTIQ	355	
Qy	361	SRPITGGGLNTTHGSGTNTSINPVLSPFSDRVVYTESYAGVLLWGIYLEPIHGVTVPFN	420	
Db	356	SRPITGGGLNTTHGSGTNTSINPVLSPFSDRVVYTESYAGVLLWGIYLEPIHGVTVPFN	415	

Query Match 53.0%; Score 3433.5; DB 2; Length 1165;
Best Local Similarity 57.4%; Pred. No. 2.4e-210;
Matches 703; Conservative 141; Mismatches 273; Indels 107; Gaps 22;

QY 40 CIARENNINPLVASTVQTGTINAGRTLVGLG-----VPPAQIASFVSFLVGLWPRG 93
DB 14 CLSNPKEL--ILGERLSTGNTVADISGLINFLYFNFPVGGGFIYGLLELWGTGP-- 69

QY 94 RDQWEIEFLEHVEQLINQITENARNTALALRQGLGDSFRAYQOSLEDMLNDRDDARTSV 153
DB 70 -SQWDIFLAQIEQLISORIEBFAHQAIISRLGSLNLYKVVYAFSDWEKDTNPALEE 128

QY 154 LYQYTALELDPLNAPLFAIRNOEYPLLMVYQAANLHLLLRDASLPFGSEFGTSQEI 213
DB 129 MRQFNDMSALITALPLFRQVNYEALLSVYQAAHLHLSDVSVFGERWGYDTATI 188

QY 214 QRYERQVQTRDYSYCVENYNTGLNSLRGTNAASWRYNQFRDLTLGLVDLVALPSS 273
DB 189 NNRYSDLTSLIHVYTHCVDYTNQGLRLEGRFLSDWIVYNNFRQLIISVLVDIVAFPPN 248

QY 274 YDRTYPTINTSQAOLTEVYTDGATGATGVMAWNNWYNNNA-----PSFAIETAVIRSP 327
DB 249 YDRTYPTIQTATLTREVYLD-----LPFINENLSPAASYPTFSAESAIRSP 297

QY 328 HLLDFLEQLTIFSTS--SRMSATRHMTYWRGHTIQSRPIGGGLN---TSTHGSTNTSINPV 383
DB 298 HLVDLFLNSPTIIVTDSLARYA-----YMGHLVNSFRGTNTLIRSLYREGNTERPV 351

QY 384 RLSFF--SRDYYTESVAGVLLNGI--YLEPIHGVTVRNFRNPNQPTFERGTANSQRYES 441
DB 352 TITASPSVPIFTLSY-----ITGLDNSNPFVAGIEGVF-----QNTISRSYRKS GPI-- 400

QY 442 PGLQLKDSLETLPPTTERPNYESYSRSLSH---IGLISQSRVHVVPYVSWTHRSADTNT 498
DB 401 -----DSFSELPPODASVSPAIGYSHLCHATFLERISGPRIAGTVFSWTHRSASPTNE 454

QY 499 ISSDITQIPLVKSFLNLSGTSVSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYV 558
DB 455 VSPSRITQIPWYKAHTLASGASVIGKPGFTGGDILTRNSMGLTGLVTFVTFGRLPQSYI 514

QY 559 RYRYA--ASQTVLWLVTVGGSTPDQGPSTWMSANESITQSFRFAEPFVIGISAGSQ-- 614
DB 515 RFRYASVANRGSTRYSQPPS--YGISPFKTMDSAGEPLTGRSFAHTLFTPTIFPSAQE 572

QY 615 -----TAGISINNAGRTFHDFKIEFIPITATFEAYDYLERAQEAVNALFTNTNPERLK 669
DB 573 FDLYIQSGV-----YIDRIEIPVTATFEAYDYLERAKVKNVALFTSTNQLGLK 621

QY 670 TDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPD 729
DB 622 TDVTDYHIDQVSNLVACLSDEFCLDEKRELSEKVKYAKRLSDERNLLQDPNFRGINRQPD 681

QY 730 FISTNEQSNTSIIHQSEHGMWGSSENTIQEGNDVFNKENVVTLPGTFNECYPYLYOKIG 789
DB 682 -----RGWRGSDTITIQQGDDVFKNVTVLPFGTFDECIYLYLQKID 723

QY 790 ESELKATRYQLRGYIEDSODLEYILIRYNAKHETLDVPGTESVWPLSVESPIGRGEPN 849
DB 724 ESKUKATRYQLRGYIEDSODLEYILIRYNAKHEIVNVPGTSLWPLSVENQIGPCGEPN 783

QY 850 RCAPHFENWPDLCSDRGKCAHSHHFLSDIDIGCTDLHENLGVVWVFKIKTQEGHAR 909
DB 784 RCAPHLEWNPDLHCSDRGKCAHSHHFLSDIDVGTCTDLNEDLGVVWVFKIKTQEGHAR 843

QY 910 LGNLEFTEEPPLGEALSRYRAKRWKRDREKQLQLETKRVYTEAKAEVDALFVDSQYNR 969
DB 844 LGNLEFTEEPPLGEALSRYRAKRWKRDREKQLQLETKRVYTEAKAEVDALFVDSQYNR 903

QY 970 LQADTNIEMIHAADKLVHRIREAYLSLSVSIPOGVNAEIEFEELGRIITAIISLYDARNVK 1029
DB 904 LQADTNIAMIHAADKVRHRIREAYLPELSVIPGVNAAIPEELERIFTAFSLYDARNIIK 963

QY 1030 NGDFNNGLACWNVKGVHDV--QSHRSVLVPIPEAEVSVQAVRVCPGRGYILRVAYKEG 1088
DB 964 NGDFNNGLLCWNVKGVHEVEBEQNNHRSVLVPIPEAEVSVQAVRVCPGRGYILRVAYKEG 1023

QY 1089 YGECVTHIENNTDELKFNCEEEERYPTDTGTCTNDYTA---HGTAVACVSRNAGYE 1144
DB 1024 YGECVTHIENNTDELKFNCEEEERYPTDTGTCTNDYTA---HGTAVACVSRNAGYE 1081

QY 1145 DAYEVDVTASVNYKPYTEESTYTDVRRDNHCEYDGVYVYPPPLPAGYMTKELYFFETDK 1204
DB 1082 EAYGNPSPVADVASVYEKSYTDRRENPCESNRGVGYDTPLPAGVYTKELYFFETDK 1141

QY 1205 VWIEIGETEGKFIYDVSVELLME 1228
DB 1142 VWIEIGETEGTFFIVDSVELLME 1165

RESULT 5
S32645
parasporal crystal protein cryiGal - Bacillus thuringiensis
C/Species: Bacillus thuringiensis
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S32645
R/Lambert, B.
submitted to the EMBL Data Library, April 1993
A/Reference number: S32645
A/Accession: S32645
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1166 <LAMB>
A/Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:G295861; PIDN:CAA80233.1; PID:G29586
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match 53.0%; Score 3433; DB 2; Length 1166;
Best Local Similarity 57.9%; Pred. No. 2.5e-210;
Matches 693; Conservative 137; Mismatches 281; Indels 86; Gaps 19;

QY 54 STVQTGINAGILGVLPAGQIASFYSLVGLMWRGRDQWEIFLEHVEQLINQIT 113
DB 34 SQVSSGLT---RFLLEAAVPEAGPALGLFDIWGAL---GVDQMSLFLRQIEQLRQIEIT 87

QY 114 ENARNTALARLQGLGDSFRAYQOSLEDMLNDRDDARTSVLYTQYIALELDFLNAPLFA 173
DB 88 ELERNRATAILTGLSSNTLYEALREWENPNPNPASQERVTRFRLTDDAIVTGLPTLA 147

QY 174 IRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTQEIQRVYERQVQTRDYSVCVE 233
DB 148 IRNLEVNLSVYVYQAANLHLLLRDASVYFGERWGLTQANIEDLYTRLTSTNIEYSDHCR 207

QY 234 WYNTGLNSLRGTNAASWRYNQFRDLTLGVLDLVALPSPYDTHYPTINTSQAOLTEVYT 293
DB 208 WYNTGLNSLRGTNAASWRYNQFRDLTLGVLDLVALPSPYDTHYPTINTSQAOLTEVYT 263

QY 294 DAIGATGVNMAWNNWYNNAPSPSAIETAVIRSVPHLLDFLEQLTIFSTSRWSATRHMTY 353
DB 264 SPVAVAGIN-----FGLSTANVLRAHLMDFIDRVIYTN-----VRSTPY 305

QY 354 WRGHTIQSRPIGGG-----LMTSTHGSTNTSINPVL---SFFSRDYYVWYTESYAGVLLWGI 406
DB 306 WAGHEVTSRRTGQGGNEIRFPFLYGVAANAEPVTVIRPTGTDEQRQWYRARSRVVSRFS 365

QY 407 YLEPIHGVTVRNFRNPNQPTFERGTANSQRYESVGLQKDSLETLPPTTERPNYESY 466
DB 366 SQGDFSLVDVAGF-----LTIFSAVSIYANGF---GFN-TDIDEIPIEGTD--PFTGY 413

QY 467 SHRLSHLGLISQS-----RVHVYVSWTHRSADTNTISSDSITQIPLVKSFLNLSGTSV 521
DB 414 SHRLCHVGFGLASSPFFISQYARAPIFSWSHRSATLTNTIAPDVITQIPLVKAFNLHSGATI 473

QY 522 VSGPGFTGGDIIRTNVNGSVLSMGLNFNNTSLQRYVRYVYAAASQTMVLRVTVGSGSTTF 580
DB 474 VKGPGFTGGDILARTNV--GSFGDMRVNITAPLSQRVIRVIRVASTTDLQFYTNNGTNTIN 532

Db 166 HLSLLADAVFQGGWGLDIATVNNHYNRLINLHRYTECHLDYNGLENLGNTNROWS 225
Qy 252 RYNQPERDITLGLVDLVALPSPVDTRTYPTINTSAQLTREVVYTDATGATGVNNAWNNYNN 311
Db 226 RNFQRFRETLTVLDLVALFPNDARAYPIQSSQUTREIYTSVSDPSVGA----- 278
Qy 312 NAPS-PSAIETAVIRSPHLLDLEQLTIFSTSRMSATRHMTYWRGHTTQSRPIQGLMT 370
Db 279 NIPNGFNRAEFGV-RPPLMDFMNSL--FVTA--ETVRSQTVWGCHLVSSR----- 324
Qy 371 STHGSTNTSINPVRISFSS-----RDVYTESYAGVLLGIVLEIHGVP 415
Db 325 -----NTAGNPINPIYGFNPGGAIWIADEDPFPYRTLS-----DPVF--- 364
Qy 416 TVRFNRPNPQN-----TFERGANYSQYSPYSPGLQKDSSTELPPTERTPNYESYSH 468
Db 365 -VRGFGFNHYVLGVAFOQTGNTHTFRNSG--TIDSLDEIPQDQNSCAPNDVSH 421
Qy 469 RLUSHIGLI-----SQSRVHVVPVSWTHRSADRTNTISSDSITQIPLVKSFLNLSGTSV 521
Db 422 VLNHVTVFVRPGELIAGSDSWRAPMFSWTHRSADRTNIINPNIITQIPAKAHNLHSGSTV 481
Qy 522 VSGPGFTGDDIIRTNVNGLSVLWGLNFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFD 581
Db 482 VRGPGFTGDDLRTNTGTFADIRVNIITGLSQRYRVIRYASTTDLQFTRINGTSVQ 541
Qy 582 QGPPSTMSANESITSQSPRFAEPFVGISASGQ---TAGISISNNAAGTQTFHDKIERIP 638
Db 542 GNFORTMNGGLESNFTAGFTPTFPFSNAQSTFTLTQAFSN---QEVYIDRIEFPV 598
Qy 639 ITATEABYDLERAQAVNALFTNTNPRRLKTDVDYHIDQVSNLVACLSDEFCLDEKRE 698
Db 599 AEVTEAESDLERAQAVNALFTSOLGLKTNVGYHIDQVSNLVACLSDEFCLDEKRE 658
Qy 699 LLEKVKYAKRLSDERNLLQDPNFTSINKQDPFISNNEQSNFTSIHQSHGHWGSENITI 758
Db 659 LSEKVKHAKRLSKRNLQDPNFRGINRPD-----HGWGSGTDITI 700
Qy 759 QSGNDVFKENYVTLPTCFNECYPTLYOKIGSELKAYTRYQLRGVIEDSQDLELYLRY 818
Db 701 QGDDVFKENYVTLPTCFNECYPTLYOKIGSELKAYTRYQLRGVIEDSQDLELYLRY 760
Qy 819 NAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHEFWNPDLDCSCRDGKCAHSHHF 878
Db 761 NSKHEIVNVPGTGSLWPLSVENQIGPCGEPNRCAPHEFWNPDLHCSRDGKCVHSHF 820
Qy 879 SLDDIDGCTDLHENLGVWVVKIKTOEGHARLGNLEFIEBKPLLGALSRLVRBAKKWRD 938
Db 821 SLDDIDVGCCTDLNEDLGWVLIPIKIQDGHARLGNLEFIEBKPLLGALSRLVRBAKKWRD 880
Qy 939 KREKLOLETKRVYTRAKEAVDALFVDSQVNRLOADTNIGMIAADKLVHRIEAYLSLS 998
Db 881 KREKLOLETNIVYKAKESVDALFVNSQVDRLOADTNIGMIAADKLVHRIEAYLSLS 940
Qy 999 VIPGVNAEIEFELEGRIITAIISLYDARNVYKNGDFFNGLACVNWKGHVDV-QQSHRSVL 1057
Db 941 VIPGVNAEIEFELEGRIITAIISLYDARNVYKNGDFFNGLACVNWKGHVDV-QQSHRSVL 1000
Qy 1058 VIPEAEAVSQAVRCPGEGYILRVYAYKEGVEGCVTHIENNTDELKFKNCSEBEVY 1117
Db 1001 VIPEAEAVSQAVRCPGEGYILRVYAYKEGVEGCVTHIENNTDELKFKNCSEBEVY 1059
Qy 1118 PTDTCGCTNDYTAHQ-----TAVCNERNAGYDAYEVDITASVNYKPYEEETDVRDN 1173
Db 1060 PNTVTVCNBYTQGVGECTDACNVRNRYGDAYGHNFTPTVHYTTPYEEETDVRDN 1119
Qy 1174 HCEYDRGVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIIVDSVELLMEE 1228
Db 1120 PCANKGVNYPPLPAGYMTKELEYFPETDKVWIEIGETEGKFIIVDSVELLMEE 1174

JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N:Alternate names: 135K insecticidal protein
C:Species: Bacillus thuringiensis
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0241
R:Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
A:Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A:Reference number: JT0241
A:Accession: JT0241
A:Molecule type: DNA
A:Residues: 1-1176 <SHI>
A:Cross-references: UNIPROT:P02965
A:Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins
C:Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 52.7%; Score 3413.5; DB 2; Length 1176;
Best Local Similarity 56.3%; Pred. No. 4.5e-209;
Matches 698; Conservative 149; Mismatches 292; Indels 100; Gaps 24;

Qy 27 MDLSPDARIEDSLCAEGNNINP-----LVSASTVQFG---INIAGRILGLV---GVPPFAGQ 77
Db 1 MDNNPNI-----NECIPYNCLSNPEVEVLGGERIETGTPIDISLSTQPLLESEFVPGAG- 55
Qy 78 IASFSYFLVGLWLP-RGRDQWEIPLFHVYQLINQITENARTALRQLGLGDSFRAYQQ 136
Db 56 ---FVLGLVDIWIWFGSPQMDAFVLVQTEQLINQIRIESFARNQAIISRLSEGLNLYIAB 112
Qy 137 SLEWLENRDARTSVLYTVVIALELDFLNAPLFAIRNOBVPFLVMVYQAANLHLIL 196
Db 113 SFREADPTPALBEEEMRIQENDMNSALTATPLFAVQNTQVPLLSVYVQAANLHLV 172
Qy 137 RDASLFGSEFGLTSGEIQRYRQVEQTRDYSYDCEVYNTGLNSLRGTNAASWRYNQF 256
Db 173 RDVSFVGQWGFDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSRDWRYNQF 232
Qy 257 RDLTLGLVLDLVALPSPVDTRTYPTINTSAQLTREVVYTDATGATGVNNAWNNYNSP 316
Db 233 RRELTLDLVDLVALPSPVDTRTYPTINTSAQLTREVVYTDATGATGVNNAWNNYNSP 280
Qy 317 SAIEITAV---IRSPHLLDLEQLTIFSTSRMSATRHMTYWRGHTTQSRPIGCG---LNT 370
Db 281 RMAQRIRQNIHQPHLMDILANSITVT-----DVHGRFNYSWGHOITASPVGSGPEAF 335
Qy 371 STHGSTNTSINPVRISFSSRDVYTES---YAGVLLW-GIYLEPIHGVTPTVRFNPN--- 423
Db 336 PLFGNAGNAAPPVLVSLTGLGIFRTLSSPLRYRRIILGSGPNNQELFVLDTGTEFSASLT 395
Qy 424 --PQNTF--ERTANYSQYSPYSPGLQKDSSTELPPTERTPNYESYSHRLSHIGLSQS- 479
Db 396 NLPSTIYQKRGTV-----DSLDVIPPQDMSVPPRAGFSHRLSHVTLMSQA 441
Qy 480 ---RVHVPVSWTHRSADRTNTISSDSITQIPLVKSFLNLSGTSVWSPGFTGDDIIRT 535
Db 442 GAVYTLRAPTSWQHRSFAFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGDDILRR 501
Qy 536 NVNGSVLSGMLFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFDQGFPPSTMSANESIT 595
Db 502 TSPGQISTLRVNIITAPLSQRYRVIRYASTTNLQPHSTSIDGRPINQGNFSATMSSGSLQ 561
Qy 596 SQSRPFAEPFVGIS-ASCSQTAGISIS-NNAGRTQTFHDKIEPIITATPEAYDLERAQ 653
Db 562 SGSPRTVTGFTTFFNPSNGSSVFTLSARVFNESGNEVY-IDRIEFVPAEYTFEAYDLERAQ 620
Qy 654 EAVNALFTNTNPRRLKTDVDYHIDQVSNLVACLSDEFCLDEKRELLSKVKYAKRLSDER 713
Db 621 KAVNELFTSSNQIGLKTVDYHIDQVSNLVACLSDEFCLDEKRELLSKVKYAKRLSDER 680
Qy 714 NLLQDPNFTSINKQDPFISTNEQSNFTSIHQSHGHWGSENITIQEGNDVFKENYVTLP 773

Db 681 NLLQDPNPRGINRQLD-----RGMRGSDITIQGGDDVFKENYVTL 722
QY 774 GFNECYPTLYQKIGESLKYTRYQLRGYIEDSQDLIELYLRNAXHETLDVPGTESV 833
Db 723 GTFDECYPTLYQKIDESKLKYTRYQLRGYIEDSQDLIELYLRNAXHETLVNPGTSL 782
QY 834 WPLSVESPIGRGEPNRCAPHPEWNPDLDCSCRDGEKCAHSHHPSLIDIGCTDLHENL 893
Db 783 WPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHPSLIDIGCTDLNEDL 842
QY 894 GVVVFKITQDGHARLGNLEFIEBKPLLGALSRVKAERKWRDKREKLOLETKRVVTE 953
Db 843 GVVVFKITQDGHARLGNLEFIEBKPLVGALSRVKAERKWRDKREKLEWETNIVYKE 902
QY 954 AKEAVDALFVDSQYNRLQADTNIGMHAADKLVRHREAYLSELSVIPGVNAEIPFEELEG 1013
Db 903 AKESVDALFVDSQYNRLQADTNIGMHAADKLVRHREAYLSELSVIPGVNAEIPFEELEG 962
QY 1014 RIITAIISLYDARNVVKNGDFNGLACMNVKGVHDV-QQSHRSVLVIPPEAEVSQAVRV 1072
Db 963 RIITAFSLYDARNVVKNGDFNGLSCNVKGVHDVEQGNORSVLVPEAEVSQAVRV 1022
QY 1073 CPGRGYILRVTAKEGYGEGCVTIEIENNTDELKFNKCEBEVYPTDTGTCNDYTAHQ- 1131
Db 1023 CPGRGYILRVTAKEGYGEGCVTIEIENNTDELKFNKCEBEVYPTDTGTCNDYTNQE 1082
QY 1132 --GTAVCNRNAGYEDAYEVDVTASVNYKPYBEETVTVDRDNHCEYDRGVNYPPLPA 1189
Db 1083 EYGGAY-TSRNARGYEAAPSV----PADYASVYSEKSYTDGRENPCBFNRYRDTPLPV 1137
QY 1190 GYMTKELEYFPETDKVWIEIGETGKFIVDSVELLMEE 1228
Db 1138 GYMTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE 1176

RESULT 10
A42459
Paraasporal crystal protein cryiFal - Bacillus thuringiensis (strain aizawai)
N:Alternate names: paraasporal crystal protein cryIF
C:Species: Bacillus thuringiensis
C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: A42459
R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-3976, 1991
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene frc
A:Reference number: A42459; MUID:91286178; PMID:2061280
A:Accession: A42459
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <CHA>
A:Cross-references: UNIPROT:Q03746; GB:M63897; NID:g142757; PIDN:AAA22348.1; PID:g142758
C:Superfamily: paraasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 52.7%; Score 3412.5; DB 2; Length 1174;
Best Local Similarity 58.4%; Pred. No. 5.2e-209;
Matches 693; Conservative 132; Mismatches 271; Indels 91; Gaps 21;
QY 72 VPPAGQIASFVSFLVGLMPPRGDQWEIFLHVLEQLNQIQTENARTALRQLGDSF 131
Db 49 VPGVGAFGLFDLIWGFIPT---SDSLFLQLEQLRIETLERNRAITTLRGLADSY 105
QY 132 RAYQOQSLDLEWLRDADRSLVLYTOYIALELDFLAMPFAIRNOBVLPLMYYAQAANL 191
Db 106 EYIEALREWEANPNNAQLREDVRIRFANTDDALITAINFTLTSFEIPLLSVYVQAANL 165
QY 192 HLLILDRASLFGSEFGLTSEIQRYRYERQVEQTRDVSQYCEWYNTGLNSLRGTNAASV 251
Db 166 HLLILDRASVFGQGWGLDIAVANNHYNRLINLHRYTKHCLDTYNOGLENLRGTRNTQWA 225
QY 252 RYNOFRDLTLGLVLDLVALPSPDYDTRYTPINTSAQLTREYVYTDAGATGNWASMMWYNN 311
Db 226 RFNOFRDLTLVLDLVALPFDVRYTPYPTQTSQTLREIYTSVIEDSPVSA----- 278

QY 312 NAPS-FSAIETAVIRPHLLDFLEQLTIFSTSSRWASATRHMTYVRGHTIQSRPIGGG-LN 369
Db 279 NIPNGFNRAEFGV-RPHLMDFNLSL--FVTA---ETVRSQTVMGHLVSRNATAGNRIN 332
QY 370 TSHGTSNTSINPRLSPFFS-----RDVYWTESYAGVLLMGYILEPIHGVTFRFNPFPQ 425
Db 333 FPSYG-----VFNPGGAIWIADEDRPFPYRTLS-----DPVP-----VRGGFGNPH 373
QY 426 N-----TPEGTANYSQPYESPGQLKDXSETLPEPETERPNYSYSYSHLSHI----- 473
Db 374 YVLGRGVAFOQTGTHRTFRNSG--TDSLDEIIPQDNGAPMNDYSHLVNHFVVRW 431
QY 474 -GLISOS-RVHPVYSWTHRSADRTNTISDSITQIPLVKSFNLNLSGTSVVSQPGTGGD 531
Db 432 PGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGTGGD 491
QY 532 IIRTNVNGSVLSMGLNFNNTSLQRYRVRYAASQTMVLAVTVGGSTTTDQGGPSTMSAN 591
Db 492 ILRRTSGGPPAYTVININGQLPQRYRARIYASTTNLRIYTVTVAGERIFAGQFNKMTDTG 551
QY 592 ESLSQSFRPAEPFVPGISASGSQTAGISISNNAGROTF-----HFDKIEFIPITAFEA 645
Db 552 DPLTFQSFVATINTAFTFMSQS-----SFTVGADTFSSGNEVYIDRFELIPVTAIFEA 606
QY 646 EYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDSEFCLDEKRELEKVKY 705
Db 607 EYDLERAQAVNALFTSIQIGIKTDVTDYHIDQVSNLVCLSDSEFCLDEKRELEKVKH 666
QY 706 AKELSDERNLLQDPNFTSINKOPDFTSTNEQSNFTSIHQSBHGWGSENIITQEGNDVF 765
Db 667 AKELSDERNLLQDPNFGINRQLD-----RGMRGSDITIQRGDDVF 708
QY 766 KENYVTLPGTFNECYPTLYQKIGESLKYTRYQLRGYIEDSQDLIELYLRNAXHETL 825
Db 709 KENYVTLPGTFDECYPTLYQKIDESKLKYTRYQLRGYIEDSQDLIELYLRNAXHEIV 768
QY 826 DVPGTESVPLSVESPIGRGEPNRCAPHPEWNPDLDCSCRDGEKCAHSHHPSLIDIG 885
Db 769 NVLGTSLMPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHPSLIDIVG 828
QY 886 CTDLHENLGVVVFVKITQDGHARLGNLEFIEBKPLLGALSRVKAERKWRDKREKLOL 945
Db 829 CTDLNEDLDVWIFKIKTDQDGHARLGNLEFIEBKPLVGALSRVKAERKWRDKREKLEL 888
QY 946 ETKRVYTEAKEAVDALFVDSQYNRLQADTNIGMHAADKLVRHREAYLSELSVIPGVNA 1005
Db 889 ETNI VYKEAKESVDALFVNSQYDQLQADTNIGMHAADKLVRHREAYLSELSVIPGVNV 948
QY 1006 EIFEELGRIITAIISLYDARNVVKNGDFNGLACMNVKGVHDV-QQSHRSVLVIPPEWA 1064
Db 949 DIFEELKGRIFTAFPLYDARNVVKNGDFNGLSCNVNKGHDVBEQNHRHSLVVPPEWA 1008
QY 1065 EYSQAVRVCPGRGYILRVTAKEGYGEGCVTIEIENNTDELKFNKCEBEVYPTDTGTC 1124
Db 1009 EYSQAVRVCPGRGYILRVTAKEGYGEGCVTIEIENNTDELKFNKCEBEVYPTDTGTC 1068
QY 1125 NDYTAHQ---GTAVCNRNAGYEDAYEVDVTASVNYKPYBEETVTVDRDNHCEYDRGY 1181
Db 1069 NDYTAHQEYGGAY-TSRNARGYDETYGNSNVPADYASVYSEKSYTDGRRDNPCESNRGY 1127
QY 1182 VNYPLPAGYMTKELEYFPETDKVWIEIGETGKFIVDSVELLMEE 1228
Db 1128 GYTPPLPAGYMTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE 1174

RESULT 11

S32647
paraasporal crystal protein cryIbbl - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S32647
R:Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645

A:Accession: S32647

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1160 <LAW>

A:Cross-references: UNIPROT:Q45747; EMBL:222511; NID:G295863; PIDN:CAA80234.1; PID:G2958

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

```
Query Match          52.6%; Score 3411; DB 2; Length 1160;
Best Local Similarity 56.2%; Pred. No. 6.3e-203;
Matches 695; Conservative 145; Mismatches 288; Indels 108; Gaps 21;

Qy 22 NHSTQMDLSPDARIEDSLCIAEGNNINP---LVSASTVQTGTINIAGRILGVLG-----V 72
Db 4 NHQIQ-----CIPNCLSNPDAILLDAERLETGNTVADISGLINFLYSNFV 50

Qy 73 PFAGQIASFYFLVGEIWPGRDQWEIFLEHVQILNQOITENARNTALARLQGLGDSFR 132
Db 51 PGGGPIVGLLEIIMGVGP--SQWEIFLAQIEQLISQRIEFARNOAISRLGLSNYE 107

Qy 133 AYQOSLEWLENRRDARTSVLYTQYIALELDFLNPMLFAIRNOEVPFLMYAQAANLH 192
Db 108 IYTFRAWKDPSPALUREEMRTQFNVMSALIAAIFLLVRVNYEVALLSVYVQAANLH 167

Qy 193 LLLRLDASLFGSEFGLTSQEIQRVYERQVETRDYSYCVWEYNTGLNSLRGTNAASVVR 252
Db 168 LSVLRDVSYGQWGFDPATVNSRYSDLRLIHVYTHCVDTYNDGLNLSGRSLSDWVV 227

Qy 253 YNQFRRLDTLGVLDLVALPSPYDTRTYINTSAQLTRVYTD--IGATGVNMAASMWYN 310
Db 228 YNRFRRLTISVLDITAFEPNYDIEAYPIQTASQLTRVYLDLPVNETLSPPASV---- 283

Qy 311 NNAPSFAIETAVRSPLHLDFEQLTIFSSSRWSATHTMYRWGHTIQSRPIGGGLN- 369
Db 284 ---PTFSAESAILRPHLVDFLNSFTIYTD-----LASVAYMGGHVNSFRFTGTTNL 335

Qy 370 --TSTHGSTNTSINPRLSFF--SRDVYWTESVAGVLLMGI-YLEPIHGVPTRVFNRPQ 425
Db 336 IRSPLYGREGNTERPVTISASPSVPIFTLSV-----FTGLNNPNVAGIEGVEP-----Q 386

Qy 426 NTFERGTANYQPVESPGQLQKDSSTELPPTTERPNYESYSHRLSH---IGLSQSRVH 482
Db 387 NTISRSIVYKSGPI-----DSPSELPPQDVSVSPAIGYSHRLCHATFLERISGPRIA 438

Qy 483 VPVYSWTHRSADRTWTISDSITQIPLYKSNLNSGTSVWSGPGTGGDITRTNVNGSVL 542
Db 439 GTVPFSWTHRSASPINEVSPSRITQIPWYKAHTLASGASVIRKPGPGTGGDILTRNSMGDLG 498

Qy 543 SMGLNFNNTSLQVRVRVRYA--ASOTVVLRTVCGSTTFDQGPSTWSANESLTSQSRF 600
Db 499 ALRVTFTGLRQSYVIRFRYASVANRSTFRYSQPPS--YGISPFTMDAGEALTSRFA 556

Qy 601 FAPFPVIGISASGQ-----TAGISINNAGROTFFDKIEPIPIPTAFAYDLERAQ 653
Db 557 HTTLFTPIFSAQOEFDLXIYQSGV-----YIDRIEFTPVDTAFESINLERAQ 605

Qy 654 EAVNALFTNTWPRRLKTDVTDYHIDQVSNIVACLSDFECLDEKRELEKVKYAKRLSDER 713
Db 606 KAVNALFTSTNLQGLKTDVTDYHIDQVSNLVECLSDFECLDEKRELEKVKYAKRLSDER 665

Qy 714 NLLQDPNFTSINKOPDFTSTNEQSNFTSIHQSEHGWMGSGENITIQEGNDVFKENYVTL 773
Db 666 NLLQDPNFRGNRQPD-----RGWRGSDITIIYQGGDDVFKENYVTLT 707

Qy 774 GTFNECYPTYLYQKIGSELKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETLDPVGTESV 833
Db 708 GTFDECYPTYLYQKIDESKLKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNVPGTSSL 767

Qy 834 WPLSVESPIGCGEPPNRCAPHENPDLDCSCRDEKCAHSHHFSFLDIDCGTDLNENL 893
Db 768 WPLSVQSPIGKCGEPPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSFLDIDVGCTDLNEDL 827
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Qy 894 GVVVVFKIQTQEGHARLGNLEFIBEKPLLGALSRVKRAEKKWRDKREKLOLETKRVYTE 953
Db 828 GVVVFIKIQDGHARLGNLEFLEBEPVLEALARVKAEEKWRDKREKLELETVIVYKE 887

Qy 954 AKEAVDALFVDSQVNRQLQADTNIGMHAADKLVHRIEAYLSIELSVIFGVNAIEFEELEG 1013
Db 888 AKESVDALFVNSQVDQLQADTNIAHAAKRVHSIRREAYLPESLVIPIGVNAGIEELEG 947

Qy 1014 RIITAIISLYDARNVVKNGDFNNGLACNVKGVVDV-QQSHRSVLVIPEWEAEVSQAVRV 1072
Db 948 RIFTAYSILYDARNVVKNGDFNNGLSCWNVKGVVDVEBQNNHRSVLVPEWEAEVSQAVRV 1007

Qy 1073 CPGRGYILRVYAYKEGEGCVTTHEINNTDELKFKNCBEEVYPTDTGTCDNDYTAHQG 1132
Db 1008 CPGRGYILRVYAYKEGEGCVTTHEVDNNTDELKFSNCEKEQVYPGNTVACNDYKXHG 1067

Qy 1133 TAVCNRNAGYEDAYEDVTTASVNYKPYEBEYTVDRDNHCEYDRGVNYPPLPAGYM 1192
Db 1068 ANACSSRNRGYDESVESNSSIPADYAPVYBEAYTDGQRNCPBFNRGHT---PLPAGYV 1124

Qy 1193 TKELEYRPETDKVWIEIGETEGKFIQVDSVELLMEE 1228
Db 1125 TAELEYRPETDVWVEIGETEGTFIVDSVELLMEE 1160
```

RESULT 12

JC2219

Parasporal crystal protein cryIIa - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*

C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: JC2219

R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.

Biosci. Biotechnol. Biochem. 58, 830-835, 1994

A:Title: Cloning of a new cryIIa(a) gene from *Bacillus thuringiensis* strain FU-2-7 and an

A:Reference number: JC2219; MUID:94289859; PMID:7764972

A:Accession: JC2219

A:Molecule type: DNA

A:Residues: 1-1176 <UDA>

A:Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:G506190; PIDN:BAA04468.1; PID:G53537

C:Genetics:

A:Gene: cryIIa(a)

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

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Query Match          52.6%; Score 3405.5; DB 2; Length 1176;
Best Local Similarity 56.3%; Pred. No. 1.5e-208;
Matches 697; Conservative 149; Mismatches 293; Indels 100; Gaps 24;
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Qy 27 MDLSPDARIEDSLCIAEGNNINP---LVSASTVOTG---INIAGRILGVL---GVPPFAGQ 77
Db 1 MDNPNIT---NECIPNCLSNPEVEVLGGERISTGTPIDISLSTQFLSEFPVPGAG- 55

Qy 78 IASFSYFLVGLWLP-RGRDQWEIFLEHVQILNQOITENARNTALARLQGLGDSFRAYQQ 136
Db 56 ---FVLGLVDIIMGIFGFSQWDAFLVQIQINRIEISFARNQAIISRLGLSNLYQIAE 112

Qy 137 SLEMDLENRDDARTSVLYTQYIALELDFLNPMLFAIRNOEVPFLMYAQAANLHLLL 196
Db 113 SFREWEADPTNPALUREEMRIQFNDMNSALTTAIFLLAVQNVQVPLLSVYVQAANLHLSVL 172

Qy 197 RDASLFGSEFGLTSQEIQRVYERQVETRDYSYCVWEYNTGLNSLRGTNAASVVRYNQF 256
Db 173 RDVSVFQWRGFDATINSRNDLTRIGNYTDVAVRWYNTGLERVWGPDSDRDVRYNQF 232

Qy 257 RRDLTGLVLDLVALPSPYDTRTYINTSAQLTRVYTDATGATGVNMAWMNWNNAAPSP 316
Db 233 RRELTLVLDLVALFNSYDSRRYPIRTVSQLTREIYTNPV-----LENFDCGSF 280

Qy 317 SAIEAV---IRSHLLDFLEQLTIFSTSSRWSATHTMYRWGHTIQSRPIGGG---LNT 370
Db 281 RGMARIBQNIQPHLMDILNSITTYT-----DVHGFNYSWGHOITASPVGSGPEFAP 335
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A;Title: Transcriptional and translational start sites for the Bacillus thuringiensis ch
A;Reference number: A92410; MUID:83109004; PMID:6296116

A;Accession: A03489

A;Molecule type: DNA

A;Residues: 1-76, 'P', 78-147, 'L', 149-247, 'S', 249-282, 'M', 284-285, 'R', 287-288, 'QN', 291-292

A;Experimental source: strain HD-1

C;Comment: This protein is present in crystalline form as a component of the spore coat.

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

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Query Match      52.5%; Score 3399.5; DB 1; Length 1178;  
Best Local Similarity 56.7%; Pred. No. 3.5e-208;  
Matches 704; Conservative 148; Mismatches 287; Indels 102; Gaps 26;  
  
QY 27 MDLSPDARIEDSLCAEGNNINP---LVSASTVQTG---INTAGRIILGV---GVPPFAGQ 77  
DB 1 MDNPNFI---NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAG- 55  
  
QY 78 IASFYSFLVGEIWP-RGRDQWEIFLEHVEQLINQOITENARTALARIQGLGDSFRAYQQ 136  
DB 56 ---FVLGLVDIIIGIFGPSOWDAFLVQIEQLINQRIEFARNQALISRLGLESLNYQIYAE 112  
  
QY 137 SLEADLENRDDARTSVLYTQVIALELDFLNMPLFAIRNOEVPPLMYAQAANLHLLL 196  
DB 113 SPREADPTNPALREEMRIQDNMNSALTTAIPLEFAVQNTQVPLLSVYVQAANLHLSVL 172  
  
QY 197 RDASLFGSEFGLTSQBIQRYERQVEQTRDYSYCVWYNTGLNSLGTNAASVVRYNQF 256  
DB 173 RDVSFVGQRMGDAATINSRYNDLTRIGNTYDVAWRWINTGLRVRWGPSDRDVRYNQF 232  
  
QY 257 RDRLTLGVLDLVALPFSYDTRYPINTSAQLTREYITDAIGATGVNMASNMWYNNAPSF 316  
DB 233 RRELTLTVLDI VALFPNDSSRRYPRTVSQLTREIYT-----NPVLENFDCSPGSA 284  
  
QY 317 SAIEATVIRSPHLLDFLQTLFISSSRWASATRWYTWRIGHTIOSRPIGGG---LNTSTH 373  
DB 285 QCIEIS-IRSPHLMILMSITIIYT-----DAHGYYYWSHGQIMASPVFGSPGPEFTPLY 338  
  
QY 374 GSTNTSINPVL-SFFSRDVTWTSYAGVLLWGLYLEPIHGVTVRNFRNPQ-----N 426  
DB 339 GTMGNAAPQQRIVAGLGGQVYRTLST-----LYRRPFN-----IGINNQLSVLDGT 386  
  
QY 427 TFERGTANY--SQVYESGLQDKSETELPETTERPNYESYSHRLSHIGLI-----S 477  
DB 387 EFAGTSSNLSAVTRKSG--TVDSLDEIPEQNNVPPRQGFSHRLSHVSMFRSGFSNS 444  
  
QY 478 QSRVHPVYVSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVVGSGPFTGGDIIRTNV 537  
DB 445 VSIIRAPMFWIHRSAEFNNIIASDSITQIPAVKGNFLNG-SVIGSGPFTGGDLVRLNS 503  
  
QY 538 NGS-----VLSMGLNFNTSLQRYRVRYAASQTMVLRTVYGGSTTFDQFPFSTMSAN 591  
DB 504 SGNNIQNRGYIEVPIHFPTS-TRYRVRYASVTP IHLNVNNGNSSIFNTVPATATSL 562  
  
QY 592 ESLTSQGFRAEFPVGSISAGSQTAGISISNAGRQTFHFEDKIEPIPTATFAEYDLER 651  
DB 563 DNLQSSDFGYPESANATSSLGNIVG--VRNFSGTAGVIIDREFIPIVPTATLEAEYNLER 620  
  
QY 652 AQEAVNALFTNTPRRLKTDVTDYHIDQVSNLVACLSDDEFCLDEKLEKLVKAKRLSD 711  
DB 621 AQKAVNALFTSTNQLGLKNTVDYHIDQVSNLVTYLSDEFCLDEKLEKLVKAKRLSD 680  
  
QY 712 ERNLQDPNFTSNKQDPDPISTNEQSNFTSIHQSEHGHWGNSNIITIQSGNDVFKENYVT 771  
DB 681 ERNLQDSNFKDINRQF-----ERGMGGSTGITIQGGDDVFKENYVT 722  
  
QY 772 LPGTFNECYPTLYLQKIGSELKAYTRYQLRGYIEDSQLEIYLIHYNAKHETLDVPGTE 831  
DB 723 LSGTFDECYPTLYLQKIDESKLKAFTRYQLRGYIEDSQLEIYLIHYNAKHETVNVPGTG 782  
  
QY 832 SVMPLSVESPIGRGCBPNCAPHFENPDIDCSRDGEKCAHHSHHFSLDIDIGCTDLHE 891  
DB 783 SLWPLSAQSPIGKCBPNCAPHLEWNPDLDCSRDGEKCAHHSHHFSLDIDVGCCTDLNE 842
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Search completed: November 21, 2004, 17:02:15

Job time : 47 secs

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QY 892 NLGVVWVFKIKTQSGHARLGNLSEIEKPLLGALSRVKDAEKKWRDKREKLQLETKRVY 951  
DB 843 DLGVWVTFKIKTQGHARLGNLSEIEKPLVGBALARKVKAACKWRDKREKLEWETNIVY 902  
  
QY 952 TEAKAVDALFVDSQYNRLQADTNIGMIHAADKLVRHIREAYLSLSVIFGVNAEIFEEL 1011  
DB 903 KEAKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLVIFGVNAEIFEEL 962  
  
QY 1012 EGRITITAIISLYDARNVVKNGDFNGLACVNVKGVHDV-QQSHHRSVLVIPWEAEVSQAV 1070  
DB 963 EGRIFTAFSLYDARNVVKNGDFNGLSCVNVKGVHDVVEEQNQNSVLPVPEWEAEVSQEV 1022  
  
QY 1071 RVCPRGYILRTVAYKEGYGEGCVTITHEIENNTDELKFNCEEEVYPTDTGTGTCNDYTAH 1130  
DB 1023 RVCPRGYILRTVAYKEGYGEGCVTITHEIENNTDELKFNCEEEVYPTDTGTGTCNDYTVN 1082  
  
QY 1131 Q---GTAVCMNSRAGYEDAYEVDVTTASVNYKPTYEEETTDVRRDNHCEYDRGVVNPPL 1187  
DB 1083 QEEYGGAY-TSRNRGYNEAPSV---PADYASVYEEKSVTDGRRENPCFENRGYRDYTPL 1137  
  
QY 1188 PAGYMTKELEYPPETDKVWIEIGETEGKEFIVDSVELLME 1228  
DB 1138 PVGYVTKELEYPPETDKVWIEIGETEGTFIVDSVELLME 1178
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2004, 09:24:41 ; Search time 153 Seconds

(without alignments)
4618.040 Million cell updates/sec

Title: US-10-614-524-2

Perfect score: 6479

Sequence: 1 LTSNRKNEINEINALSPAV.....IGETEGKFIQVDSVLLMEE 1228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5924.5	91.4	1227	1 C1BB_BACTU	O85805 bacillus th
2	5745	88.7	1228	1 C1BA_BACTK	P05517 bacillus th
3	5740	88.6	1228	2 Q93T75	O93t75 bacillus th
4	5737	88.5	1228	2 Q93NM5	O93nm5 bacillus th
5	5235.5	80.8	1229	1 C1BB_BACTU	O45739 bacillus th
6	5214.5	80.5	1231	1 C1BD_BACTZ	Q9zaz5 bacillus th
7	5188.5	80.1	1231	2 Q8KNY2	O8kny2 bacillus th
8	4959.5	76.5	1233	1 C1BC_BACTM	O45774 bacillus th
9	4284.5	66.1	1215	1 C1CA_BACTM	O45715 bacillus th
10	3977.5	61.4	1174	1 C1EB_BACTA	O03745 bacillus th
11	3901.5	60.2	849	2 Q6PYW8	O6pyw8 bacillus th
12	3901.5	60.2	849	2 AAS93797	Aas93797 bacillus
13	3791	58.5	1176	1 C1CB_BACTG	P56953 bacillus th
14	3579	55.2	1170	1 C1JB_BACTU	O45716 bacillus th
15	3556	54.9	1167	1 C1JA_BACTU	O45738 bacillus th
16	3495.5	54.0	1189	1 C1CA_BACTE	P05518 bacillus th
17	3495.5	54.0	1189	2 O6YNE8	O6ymb8 bacillus th
18	3495.5	54.0	1189	2 AAM00264	Aam00264 bacillus
19	3495.5	54.0	1189	2 AAL79362	Aal79362 bacillus
20	3455.5	53.8	1189	2 Q91877	Q91877 bacillus th
21	3455.5	53.3	1180	2 Q9S5V8	Q9s5v8 bacillus th
22	3433.5	53.0	1165	1 C1DA_BACTA	P19415 bacillus th
23	3433	53.0	1166	1 C1GA_BACTU	O45746 bacillus th
24	3428	52.9	1179	1 C1AD_BACTL	Q03744 bacillus th
25	3426.5	52.9	1181	1 C1AB_BACTL	Q03748 bacillus th
26	3426	52.9	1171	2 O06894	O06894 bacillus th
27	3426	52.9	1171	2 Q71TW6	Q71tw6 bacillus th
28	3426	52.9	1171	2 AAL50330	Aal50330 bacillus th
29	3425	52.9	1177	2 Q6EIX3	Q6eix3 bacillus th
30	3421	52.8	1171	1 C1EA_BACTX	Q57458 bacillus th
31	3413.5	52.7	1174	2 Q45749	Q45749 bacillus th

ALIGNMENTS

RESULT 1

ID	C1BB_BACTU	STANDARD;	PRT;	1227 AA.
AC	O85805;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Pestigical crystal protein cryIbE (insecticidal delta-endotoxin			
DE	CryIbE(e)) (Crystalline entomocidal protoxin) (139 kDa crystal protein).			
GN	Name=cryIbE; Synonyms=cryIB(e), 158C2B;			
OS	Bacillus thuringiensis.			
OG	Plasmid pMYC2383.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1428;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NREL B-19872 / PS158C2;			
RA	Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Steiman S.;			
RT	"Bacillus thuringiensis genes encoding lepidopteran-active toxins.";			
RL	Patent number US5723758, 03-MAR-1998.			
CC	-!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae.			
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.			
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.			
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; AF077326; AAC32850.1; -.			
DR	HSSP; P07130; 1DLC.			
DR	InterPro; IPR001178; Endotoxin.			
DR	InterPro; IPR005638; endotoxin_C.			
DR	InterPro; IPR005639; endotoxin_N.			
DR	InterPro; IPR008979; Gal_bind_like.			
DR	Pfam; PF03944; Endotoxin_C; 1.			
DR	Pfam; PF00555; Endotoxin_M; 1.			
DR	Pfam; PF03945; Endotoxin_N; 1.			
KW	Plasmid; Sporulation; Toxin.			
SQ	SEQUENCE 1227 AA; 139084 MW; CBA847BEA0B34CD3 CRC64;			

Query Match 91.4%; Score 5924.5; DB 1; Length 1227;

Best Local Similarity 91.7%; Pred. No. 0;

Matches 1128; Conservative 37; Mismatches 60; Indels 5; Gaps 3;

OY 1 LTSNRKNEINEINALSPAVNSHNHSTQMDLSPDARIEDSLCTAEGNNINPLVSASTVQTGI 60

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Db 1 MTNRKNEIINALSIPAVNSHAQMLSTDAIEDSLCAEGNIDPFVSASTVQTGI 60
QY 61 NIAGRILGLVGPAGQIASFYSFLVGLWPRGRDQWEIFLEHVEQLINOQITENARNTA 120
Db 61 NIAGRILGLVGPAGQIASFYSFLVGLWPRGRDPWEIFLEHVEQLIROQVIENTADTA 120
QY 121 LARLOGLGDSFRAYQOQSLEDWLENRDDARTSVLYTYQVIALELDFLNAFLPFAIRNQVEP 180
Db 121 LARLOGLGDSFRAYQOQSLEDWLENRDDARTSVLYTYQVIALELDFLNAFLPFAIRNQVEP 180
QY 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQIOIYRYERQVQTRDYSDYCVHYWYNTGLN 240
Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQIOIYRYERQVQTRDYSDYCVHYWYNTGLN 240
QY 241 SLRGTNAASVRYNQFRDLTLGLVLDLVALFPSPDYTRTYPINTSAQLTREYVYTDAGATG 300
Db 241 NLRGTAESWLRYNQFRDLTLGLVLDLVALFPSPDYTRTYPINTSAQLTREYVYTDAGATG 300
QY 301 V--NWASNNWYNNAPSAFSAIETAVIRSPHLLDFLEQLTTFSTSSRWASRTHMYWRIGHT 358
Db 301 APSGFATSNWNNAPSAFSAIETAVIRSPHLLDFLEQLTTFSTSSRWASRTHMYWRIGHT 358
QY 359 IQSRPIGGGLNTSTHGSTNTSINPVRLSFRSDRVYMTESVAGVLLGWILYLEPIHGVPVTR 418
Db 361 LESRTIRGLSTSTHGSTNTSINPVRLSFRSDRVYMTESVAGVLLGWILYLEPIHGVPVTR 418
QY 419 FNFNPQNTFERGTANTYQPYESFGLQKDSLETLPPTERRPNYESYSHRLSHIGLISQ 478
Db 419 FNFNPQNTFERGTANTYQPYESFGLQKDSLETLPPTERRPNYESYSHRLSHIGLISQ 478
QY 479 SRVHVPLYWTHRADTNTISSDSITQIPLVKSFNLSGTSVVGPGFTGGDIIRTNVN 538
Db 479 SRVHVPLYWTHRADTNTISSDSITQIPLVKSFNLSGTSVVGPGFTGGDIIRTNVN 538
QY 539 GSVLSMGLNFNTSLQRYRVRVYAAQOTWLVRYVVGSTTFDQPPSTWSANESLTSQS 598
Db 539 GSVLSMGLNFNTSLQRYRVRVYAAQOTWLVRYVVGSTTFDQPPSTWSANESLTSQS 598
QY 599 FRAPFPVGSASQGTAGISINNAGRTQFHFQKIEFIPITATFEAYDLERAQAVNA 658
Db 599 FRAPFPVGSASQGTAGISINNAGRTQFHFQKIEFIPITATFEAYDLERAQAVNA 658
QY 659 LFTNTNPRRLKTDVTHIDOVSNLVAQLSDECLDEKRELLKVKYAKLSDERNLLQD 718
Db 659 LFTNTNPRRLKTDVTHIDOVSNLVAQLSDECLDEKRELLKVKYAKLSDERNLLQD 718
QY 719 PNFTSINKQPDFISTNEQSNFTSIHQSEHGWSGSENIITIQEGNDVPKENYVTLPGTFNE 778
Db 719 PNFTSINKQPDFISTNEQSNFTSIHQSEHGWSGSENIITIQEGNDVPKENYVTLPGTFNE 778
QY 779 CYPYLYQKIGESLKYATRYQLRGYIEDSQDLIEYLIRYNNAKHETLDVPGTSEVWPLSV 838
Db 779 CYPYLYQKIGESLKYATRYQLRGYIEDSQDLIEYLIRYNNAKHETLDVPGTSEVWPLSV 838
QY 839 ESPIGRCGEPNRCAPHEWNPDDCSRDCEKCAHSHHFSLDIDIGCTDLHENLGVWVY 898
Db 839 ESPIGRCGEPNRCAPHEWNPDDCSRDCEKCAHSHHFSLDIDIGCTDLHENLGVWVY 898
QY 899 FKIKTQEGHARLGNLEPIERKPLLEALSRVYKRAEKKWRDKREKLQLETRKRVYTEAKEAV 958
Db 899 FKIKTQEGHARLGNLEPIERKPLLEALSRVYKRAEKKWRDKREKLQLETRKRVYTEAKEAV 958
QY 959 DALFVDSQVNRLOADNTNIGMHAADKLVRIRAYLSLSVIVGVNAEIPFEELGRIITA 1018
Db 959 DALFVDSQVNRLOADNTNIGMHAADKLVRIRAYLSLSVIVGVNAEIPFEELGRIITA 1018
QY 1019 ISLYDARNVYKNGDFNNGLACMNVKGVHDVYQOQSHRSVLVPEWEAEVSOAVRCPGRGY 1078
Db 1019 ISLYDARNVYKNGDFNNGLACMNVKGVHDVYQOQSHRSVLVPEWEAEVSOAVRCPGRGY 1078
QY 1079 ILRVYAYKEGYGGCVTIHIEIENNTDELKPKNCEEEVYPTDGTGTCNDYTAHQGTACVNS 1138
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1078 ILRVYAYKEGYGGCVTIHIEIENNTDELKPKNCEEEVYPTDGTGTCNDYTAHQGTACVNS 1137
1139 RNAGYEDAVEVDVTASVNYKYPTVEETYYDVRDNHCEYDRGVYVNPPLPAGYMTKELEY 1198
1138 RNAGYEDAVEVDVTASVNYKYPTVEETYYDVRDNHCEYDRGVYVNPPLPAGYMTKELEY 1197
1199 FPETDKVWISIGTEGKFIVDSVELLMEE 1228
1198 FPETDKVWISIGTEGKFIVDSVELLMEE 1227

RESULT 2
C1BA BACTK
ID C1BA BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbA (insecticidal delta-endotoxin
DE CryIb(a)) (crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Names=cryIbA; Synonyms=cryIb(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria, Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
SEQUENCE FROM N.A.
RP SPECIES=B.t.kurstaki; STRAIN=HD-2;
RC MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723 (1988).
RN [2]
SEQUENCE FROM N.A.
RP SPECIES=B.t.entomocidus; STRAIN=HD-110;
RC Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; X06711; CAA29898.1; -.
CC EMBL; X95704; CAA65003.1; -.
CC F01; S00873; S00873.
CC HSP; P07130; 1DLC.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 13647 MW; C8E3A19F85D98575 CRC64;

Query Match 88.7%; Score 5745; DB 1; Length 1228;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1098; Conservative 35; Mismatches 90; Indels 10; Gaps 3;
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QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MTSNRKNEIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55

61 NIAGRILGLVGPVFPAGQIASFYSFLVGLWPRGRDQWEI FLEHVQLNQITENARNTA 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 NIAGRILGLVGPVFPAGQIASFYSFLVGLWPRGRDQWEI FLEHVQLNQITENARNTA 115

121 LARLQGLGDSFRAYCOQSLDLEWLRDARTSVLTYQIALELDFLNAMPFAIRNQVVP 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 LARLQGLGDSFRAYCOQSLDLEWLRDARTSVLTYQIALELDFLNAMPFAIRNQVVP 175

181 LLMYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWNTNGLN 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 LLMYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWNTNGLN 235

241 SLRGTNAASWVRYNQFRDLTLGVLDLVALPSPYDTRTPINTSAQLTRVYTDAGATG 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
236 SLRGTNAASWVRYNQFRDLTLGVLDLVALPSPYDTRTPINTSAQLTRVYTDAGATG 295

301 VNMAASWVRYNQFRDLTLGVLDLVALPSPYDTRTPINTSAQLTRVYTDAGATG 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
296 VNMAASWVRYNQFRDLTLGVLDLVALPSPYDTRTPINTSAQLTRVYTDAGATG 355

361 SRPIGGGGLNTSTHGSTNTSINPVRLSFFSRDVTWYTESYAGVLLWGIYLEPIHGVPTRFN 420
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356 SRPIGGGGLNTSTHGATNTSINPVTLRPASRDVYRTESYAGVLLWGIYLEPIHGVPTRFN 415

421 FRNPONTERTGANTYQSPYSPGLQKDSSETLPPETTERPNYESYSHRLSHIGLISQSR 480
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
416 FTNPQNSIDRGNTANTYQSPYSPGLQKDSSETLPPETTERPNYESYSHRLSHIGLISQSR 475

481 VHPVYVSWTHSADRTNTISDLSITQIPLVKSFNLNGTSVVSQPGFTGGDIIRTNVNGS 540
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476 VNPVYVSWTHSADRTNTIGNRITQIPWVKAELPQGTTVVRGPGFTGGDILRNTTGG 535

541 VLSGLNFNTSLQRYRVRYAASQTMVLRVTVGGSTTFQCGFSTMSANESLTSQSFR 600
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
536 FGPIRVTVNGPLTQRYRGFRYASTVDFPFVSRGGTTVNNFRFLRTWNSGDELKYGNFV 595

601 FAPVPVGISAGSQ-TAGISISNAGROTTFPKIEPIPTATPAEYDLERAQAVNAL 659
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
596 RRAFTPTPTQIQDIIRTSIQGLSGNGEVTDKIEIIPVTATPAEYDLERAQAVNAL 655

660 FTNTNPRLKTDDVTDYHIDQVSNLVACLSDFCLDEKELLEKKVYAKRLSDERNLLQDP 719
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656 FTNTNPRLKTDDVTDYHIDQVSNLVACLSDFCLDEKELLEKKVYAKRLSDERNLLQDP 715

720 NFTSINKQDPFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNEC 779
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716 NFTSINKQDPFISTNEQSNFTSIHQSEHGWMGSENITIQEGNDVFKENYVTLPGTFNEC 775

780 YPTVLYQKIGSELKAYTRYQLRGYIEDSQLEIYLIRYNAKHETLDVPGTESVWPLSV 839
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
776 YPTVLYQKIGSELKAYTRYQLRGYIEDSQLEIYLIRYNAKHETLDVPGTESVWPLSV 835

840 SPIGCEGPNRCAPHFENPDLDCSROGCEKCAHSHHFSLDIDIGCTDLHENLGVWVVP 899
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
836 SPIGCEGPNRCAPHFENPDLDCSROGCEKCAHSHHFSLDIDIGCTDLHENLGVWVVP 895

900 KIKTOEGHARLGNLEFI BEKPLLGALSRVKAERKWRDKEKQLETKRVVYTAKEAVD 959
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
896 KIKTOEGHARLGNLEFI BEKPLLGALSRVKAERKWRDKEKQLETKRVVYTAKEAVD 955

960 ALFVDSQVNRLOADTNGIMHAADKLVHRIEAYLSLSVPGVNAEIFELEGGHITAI 1019
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
956 ALFVDSQVNRLOADTNGIMHAADKLVHRIEAYLSLSVPGVNAEIFELEGGHITAI 1015

1020 SLYDARNVVKGDFFNGLACWNVKGVDPQOSSHRSVLVIFEWAEVSOAVRVCPGCGYI 1079
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1016 SLYDARNVVKGDFFNGLTCWNVKGVDPQOSSHRSDLVIFEWAEVSOAVRVCPGCGYI 1075
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QY 1080 LRVTAKEGYGEGCVTIHEIENNTDELKFKNCEBEVYPTDTGTCDNTAHOQTA----V 1135
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1076 LRVTAKEGYGEGCVTIHEIENNTDELKFKNCEBEVYPTDTGTCDNTAHOQTAGCADA 1135

1136 CNSRNAGYEDAYEVDVTTASVNYKPTYEBETVTVRRDNHCEYDRGYVNYPLPAGYMKKE 1195
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1136 CNSRNAGYEDAYEVDVTTASVNYKPTYEBETVTVRRDNHCEYDRGYVNYPPVAGYVTKKE 1195

1196 LEYFPETDKWIBIGETGKFIVDSVELLMEE 1228
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1196 LEYFPETDKWIBIGETGKFIVDSVELLMEE 1228

RESULT 3
Q93T75 PRELIMINARY, PRT: 1228 AA.
ID Q93T75 AC Q93T75;
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; Endotoxin.
DR InterPro; IPR008979; Gal bind Like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_N_1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 88.6%; Score 5740; DB 2; Length 1228;
Best Local Similarity 89.0%; Pred. No. 0;
Matches 1097; Conservative 36; Mismatches 90; Indels 10; Gaps 3;

QY 1 LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MTSNRKNEIIN-----AVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55

61 NIAGRILGLVGPVFPAGQIASFYSFLVGLWPRGRDQWEI FLEHVQLNQITENARNTA 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 NIAGRILGLVGPVFPAGQIASFYSFLVGLWPRGRDQWEI FLEHVQLNQITENARNTA 115

121 LARLQGLGDSFRAYCOQSLDLEWLRDARTSVLTYQIALELDFLNAMPFAIRNQVVP 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 LARLQGLGDSFRAYCOQSLDLEWLRDARTSVLTYQIALELDFLNAMPFAIRNQVVP 175

181 LLMYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWNTNGLN 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 LLMYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVWNTNGLN 235

241 SLRGTNAASWVRYNQFRDLTLGVLDLVALPSPYDTRTPINTSAQLTRVYTDAGATG 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
236 SLRGTNAASWVRYNQFRDLTLGVLDLVALPSPYDTRTPINTSAQLTRVYTDAGATG 295

301 VNMAASWVRYNQFRDLTLGVLDLVALPSPYDTRTPINTSAQLTRVYTDAGATG 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
296 VNMAASWVRYNQFRDLTLGVLDLVALPSPYDTRTPINTSAQLTRVYTDAGATG 355

361 SRPIGGGGLNTSTHGSTNTSINPVRLSFFSRDVTWYTESYAGVLLWGIYLEPIHGVPTRFN 420
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 356 SRPIGGGLTSTHATNTSINPVLRFASRDVYVTESVAGVLLGVIILEPIHGVPVTFN 415
Qy 421 FRNPONTFERTANYSQYSPGQLKDSLETLPETTERPNYESYSHRLSHIGLISQSR 480
Db 416 FTNPQNSIDRGNTANYSQYSPGQLKDSLETLPETTERPNYESYSHRLSHIGLISQSR 475
Qy 481 VHPVYSWTHSADRTNISDSITQIPLVKSFNLSGTSVVSGPGTGGDIIRTNVNGS 540
Db 476 VNVVYSWTHSADRTNIGPNRIQIIPWKASLPQGTTVVRGPGTGGDILRRTNTGG 535
Qy 541 VLSMGLFNNTSLQRYRVRYAASQTMVLRTVVGSTTTFDQGPSTMSANESLTSQSPR 600
Db 536 FGPVRTVNGPLTQRYRIGFYASTVDFDFVSGGTTVNNFRFLRTMNSGDELKYGNFV 595
Qy 601 PAEPFVGISAGSQ-TAGISISNNAGROTQHFDFKIEIPITATFEAEYDLERAQEAVAL 659
Db 596 RRAFTPTFTTQIQDIIRTSIQGLSGNGEVYDKIEIIPVTATFEAEYDLERAQEAVAL 655
Qy 660 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCCLDEKRELEKVKYAKRLSDERNLLQDP 719
Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCCLDEKRELEKVKYAKRLSDERNLLQDP 715
Qy 720 NFTSINKQPDFISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVFKENYVTLPGTFNEC 779
Db 716 NFTSINKQPDFISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVFKENYVTLPGTFNEC 775
Qy 780 YPTLYQKIGESELKAYTRQOLRYIIRDSQDLIELYLRYNAKHETLDVPGTESWPLSVE 839
Db 776 YPTLYQKIGESELKAYTRQOLRYIIRDSQDLIELYLRYNAKHETLDVPGTESWPLSVE 835
Qy 840 SPIGRCCENRCAPHEFWNPDLDCSCRDGKCAHSHHPSLDDIGCTDLHENLGVWVVF 899
Db 836 SPIGRCCENRCAPHEFWNPDLDCSCRDGKCAHSHHPSLDDIGCTDLHENLGVWVVF 895
Qy 900 KIKTOEGHARLGNLEFIEEKPLGEALSrvKRAKRWDRKREKLQETKEVYVTEAKEAVD 959
Db 896 KIKTOEGHARLGNLEFIEEKPLGEALSrvKRAKRWDRKREKLQETKEVYVTEAKEAVD 955
Qy 960 ALFVDSQYNRLQADTNGIMHAADKLVRIRIAYLSLSVPGVNAIIPBELGRITAI 1019
Db 956 ALFVDSQYDLQADTNGIMHAADKLVRIRIAYLSLSVPGVNAIIPBELGRITAI 1015
Qy 1020 SLYDARNVKNQGNFNGLACWNVKGVHVQOQSHRSVLVPIPEAEVSOAVRVCPCRGYI 1079
Db 1016 SLYDARNVKNQGNFNGLACWNVKGVHVQOQSHRSVLVPIPEAEVSOAVRVCPCRGYI 1075
Qy 1080 LRVYAYKEGYGEGCVTTHIENNTDELKFKNCBEEVEYPTDTGTCNDYTAHQGTA---V 1135
Db 1076 LRVYAYKEGYGEGCVTTHIENNTDELKFKNCBEEVEYPTDTGTCNDYTAHQGTA 1135
Qy 1136 CNSRNAGYEDAYEDVDTTASVNYKPYEEETVTVRRDNHCEYDRGVYVPPPLPAGYVTK 1195
Db 1136 CNSRNAGYEDAYEDVDTTASVNYKPYEEETVTVRRDNHCEYDRGVYVPPVAGYVTK 1195
Qy 1196 LEYFPETDKVWIEIGETEGKFIVDSVELLIMEE 1228
Db 1196 LEYFPETDKVWIEIGETEGKFIVDSVELLIMEE 1228
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RESULT 4

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Q93NM5 ID Q93NM5 PRELIMINARY; PRT; 1228 AA.
AC Q93NM5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Cry1Ba.
GN Name=Cry1Ba;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1426;
RN [1]
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RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Iike.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF03945; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341PB439 CRC64;
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Query Match 88.5%; Score 5737; DB 2; Length 1228;
Best Local Similarity 89.0%; Pred. No. 0;
Matches 1097; Conservative 35; Mismatches 91; Indels 10; Gaps 3;

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Qy 1 LTSNRKNEIINALSIPAVSNHSTQMDLSQPARIEDSLCIAEGNNINPLVSASTVQTGI 60
Db 1 MTSNRKNEIIN-----AVSNHSAQMQLLPDARIEDSLCIAEGNNIDPFVSASTVQTGI 55
Qy 61 NIAGRIILGVLPVFPAGQIASFYSLVGLWLPGRDQWEIFLHVQLINQITENARNTA 120
Db 56 NIAGRIILGVLPVFPAGQIASFYSLVGLWLPGRDQWEIFLHVQLINQITENARNTA 115
Qy 121 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLVYQYIALELDFLNAMPLFAIRNOEVP 180
Db 116 LARLOGLGDSFRAYQOSLEDWLENRDDARTSRVLVYQYIALELDFLNAMPLFAIRNOEVP 175
Qy 181 LLMVYAAANLHLLLRDASLFGSEFGLTSQBIQRYERQVQETRDYSDYCVENYNTGLN 240
Db 176 LLMVYAAANLHLLLRDASLFGSEFGLTSQBIQRYERQVQETRDYSDYCVENYNTGLN 235
Qy 241 SLRGTTNAAWVYVNGFRRLDTLGVLDLVALFSDYTRTPYINTSAQLTREVTDAIGATG 300
Db 236 SLRGTTNAAWVYVNGFRRLDTLGVLDLVALFSDYTRTPYINTSAQLTREVTDAIGATG 295
Qy 301 VNMASNNVYNNAPFSAYETAVIRSPHLLDLEOLTTFSTSSRWSATRHMTYWRGHTIQ 360
Db 296 VNMASNNVYNNAPFSAYETAVIRSPHLLDLEOLTTFSTSSRWSATRHMTYWRGHTIQ 355
Qy 361 SRPIGGGLTSTHGTSTNTSINPVLRFASRDVYVTESVAGVLLGVIILEPIHGVPVTFN 420
Db 356 SRPIGGGLTSTHGTSTNTSINPVLRFASRDVYVTESVAGVLLGVIILEPIHGVPVTFN 415
Qy 421 FRNPONTFERTANYSQYSPGQLKDSLETLPETTERPNYESYSHRLSHIGLISQSR 480
Db 416 FTNPQNSIDRGNTANYSQYSPGQLKDSLETLPETTERPNYESYSHRLSHIGLISQSR 475
Qy 481 VHPVYSWTHSADRTNISDSITQIPLVKSFNLSGTSVVSGPGTGGDIIRTNVNGS 540
Db 476 VNVVYSWTHSADRTNIGPNRIQIIPWKASLPQGTTVVRGPGTGGDILRRTNTGG 535
Qy 541 VLSMGLFNNTSLQRYRVRYAASQTMVLRTVVGSTTTFDQGPSTMSANESLTSQSPR 600
Db 536 FGPVRTVNGPLTQRYRIGFYASTVDFDFVSGGTTVNNFRFLRTMNSGDELKYGNFV 595
Qy 601 PAEPFVGISAGSQ-TAGISISNNAGROTQHFDFKIEIPITATFEAEYDLERAQEAVAL 659
Db 596 RRAFTPTFTTQIQDIIRTSIQGLSGNGEVYDKIEIIPVTATFEAEYDLERAQEAVAL 655
Qy 660 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCCLDEKRELEKVKYAKRLSDERNLLQDP 719
Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDFCCLDEKRELEKVKYAKRLSDERNLLQDP 715
Qy 720 NFTSINKQPDFISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVFKENYVTLPGTFNEC 779
Db 716 NFTSINKQPDFISTNEQSNFTSIHQSEHGHWGSENITIQEGNDVFKENYVTLPGTFNEC 775
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QY 780 YPTLYQKIGSELKAYTRYQLRGYIEDSQLEIYLIRYNKAGHETLDVPGTESVWPLSV 839
 Db 776 YPTLYQKIGSELKAYTRYQLRGYIEDSQLEIYLIRYNKAGHETLDVPGTESVWPLSV 835
 QY 840 SPIGCGEPNRCAPHFENPDLDCSCRDGKCAHSHHFSLDIDIGCTDLHENLGVWVVF 899
 Db 836 SPIGCGEPNRCAPHFENPDLDCSCRDGKCAHSHHFSLDIDVGCTDLHENLGVWVVF 895
 QY 900 KIKTQEGHARLGNLEFIEBEKPLLEALSRVRAEKKWRDKREKQLETKRVYVTEAKBAVD 959
 Db 896 KIKTQEGHARLGNLEFIEBEKPLLEALSRVRAEKKWRDKREKQLETKRVYVTEAKBAVD 955
 QY 960 ALFVDSQVNRLOADTNGIMHAADKLVHRIEAYLSVSELSVIPGVNAEIFELEGRITAI 1019
 Db 956 ALFVDSQVNRLOADTNGIMHAADKLVHRIEAYLSVSELSVIPGVNAEIFELEGRITAI 1015
 QY 1020 SLYDARNVVRKGDENGLACNVKGVHDVQOSHRSVLVPEWEAEVSQAVRVCPCGGYI 1079
 Db 1016 SLYDARNVVRKGDENGLACNVKGVHDVQOSHRSVLVPEWEAEVSQAVRVCPCGGYI 1075
 QY 1080 LRVYAYKEGYGEGCVTHIEIENNTDELKFKNCEBEVEVPTDTGTCNDYTAHQGTA---V 1135
 Db 1076 LRVYAYKEGYGEGCVTHIEIENNTDELKFKNCEBEVEVPTDTGTCNDYTAHQGTA 1135
 QY 1136 CNSNAGYEDAYEVDVTTASVNVKPYEETVTVRRDNHCEYDRGVNYPPLPAGYMTKE 1195
 Db 1136 CNSNAGYEDAYEVDVTTASVNVKPYEETVTVRRDNHCEYDRGVNYPPLPAGYMTKE 1195
 QY 1196 LEYFPEPTDQWIEGETEGKPIVDSVELLME 1228
 Db 1196 LEYFPEPTDQWIEGETEGKPIVDSVELLME 1228

RESULT 5

C1BB_BACTU STANDARD; PRT; 1229 AA.
 ID C1BB_BACTU STANDARD; PRT; 1229 AA.
 AC Q45739;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Pesticidal crystal protein cryIbB (Insecticidal delta-endotoxin
 DE CryIbB) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
 GN Name=cryIbB; Synonyms=cryIb(b), cryET5;
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL B-21110 / EG5847;
 RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
 RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
 RT toxic to lepidopteran insects.";
 RL Patent number US5322687, 21-JUN-1994.
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
 CC epithelial cells of many lepidopteran larvae.
 CC -!- DEVELOPMENTAL STAGES: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 CC terminus.
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L32020; AAA22344.1; -;
 DR HSSP; P02965; 1CIY.
 DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin C.
 DR InterPro; IPR005639; endotoxin N.
 DR InterPro; IPR008979; Gal bind Like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 KW Sporulation; Toxin.
 SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;
 Query Match 80.8%; Score 5235.5; DB 1; Length 1229;
 Best Local Similarity 79.8%; Pred. No. 0;
 Matches 982; Conservative 95; Mismatches 149; Indels 5; Gaps 3;
 QY 1 LTSNKKNEIINALSIPAVSNHSTQMDLSDPARIEDSLCIAEGNNINPLVSASTVQTGI 60
 Db 1 MTSNKKNEIINALSIPAVSNHSTQMDLSDPARIEDSLCIAEGNNINPLVSASTVQTGI 60
 QY 61 NIAGRIILGVLPAGQIASFYSLVGLMELPRGRDQWBIPLHEVQLINQOITENARNTA 120
 Db 61 NIAGRIILGVLPAGQIASFYSLVGLMELPRGRDQWBIPLHEVQLINQOITENARNTA 120
 QY 121 LARLOGLGDSFRAYQOQSLDHLNRDDARTSVLYTOYIALELDFLNAMPLFAIRNQVVP 180
 Db 121 LARLEGLRGYRSYQOQSLDHLNRDDARTSVLYTOYIALELDFLNAMPLFAIRNQVVP 180
 QY 181 LLMYVYAQANLHLLLRDASLFGSEFGLTSQEIORYYERQVETRDRDYDCVWYNTGLN 240
 Db 181 LLMYVYAQANLHLLLRDASLFGSEFGLTSQEIORYYERQVETRDRDYDCVWYNTGLN 240
 QY 241 SLRGTNAASVRYNQFRDLTLGLVDLVALPSPYDTRTPINTSAQLFREYVTDAGATG 300
 Db 241 NLRGTNAESVRYNQFRDLTLGLVDLVALPSPYDTRTPINTSAQLFREYVTDPIGRTN 300
 QY 301 V--NMASHWYNNAPSFSAIETAVIRSPHLLDLEQLTIETSSRWGATRHMTWTRGHT 358
 Db 301 APSGFASNTMFPNNAPSFSAIETAVIRSPHLLDLEQLTIETSSRWGATRHMTWTRGHT 360
 QY 359 IQSRPIGGGLNTSTHGST--NTSINPRLSPSRDVRVYTESVAGVLLWGLIYLEPIHGVPV 417
 Db 361 LNFPIPGGLNTSTHGST--NTSINPRLSPSRDVRVYTESVAGVLLWGLIYLEPIHGVPV 418
 QY 418 RFNFRNPONTFERGTANYQSPYSGPLQKDSFETLPETTERPYESYSHRLSHIGLIS 477
 Db 419 RFNFRNPONTFERGTANYQSPYSGPLQKDSFETLPETTERPYESYSHRLSHIGLII 478
 QY 478 QSRVHVVPVSWTHRSADRTNIISSDSITOTPLVKSFNLSGTSVVSQPGTGGDIIRTNV 537
 Db 479 GNTLRAPVYSWTHRSADRTNIISSDSITOTPLVKSFNLSGTSVVSQPGTGGDIIRTNV 538
 QY 538 NGSVLSMGLNPNNTSLQRYVRVRYAASQTMVLRLVTVVGGSTTFDQGFPTMSANESLTSQ 597
 Db 539 TGTGFDIRLAINVPLSQRYVRVRYAASQTMVLRLVTVVGGSTTFDQGFPTMSANESLTSQ 598
 QY 598 SFRPAEPVGISASGQTAGISISNNAGRQTFHDKIEFIPITATFEAYDLERAQEA 657
 Db 599 SFRPAEPVGISASGQTAGISISNNAGRQTFHDKIEFIPITATFEAYDLERAQEA 658
 QY 658 ALFTNTNPRKTDVTDYHIDQVSNMVACUSDFCLDEKRELLEKVKYAKLSDBERNLQ 717
 Db 659 ALFTNTNPRKTDVTDYHIDQVSNMVACUSDFCLDEKRELLEKVKYAKLSDBERNLQ 718
 QY 718 DPNFTSINKOPDFISTNEQSNFTSIHQSEHGWSGSENITIQEGNDVPKENYVTLPGTFN 777
 Db 719 DPNFTSINKOPDFISTNEQSNFTSIHQSEHGWSGSENITIQEGNDVPKENYVTLPGTFN 778
 QY 778 ECPYTYLYQKIGSELKAYTRYQLRGYIEDSQLEIYLIRYNKAGHETLDVPGTESVWPLS 837
 Db 779 ECPYTYLYQKIGSELKAYTRYQLRGYIEDSQLEIYLIRYNKAGHETLDVPGTESVWPLS 838
 QY 838 VESPIGRGEPNRCAPHFENPDLDCSCRDGKCAHSHHFSLDIDIGCTDLHENLGVWV 897
 Db 839 VESPIGRGEPNRCAPHFENPDLDCSCRDGKCAHSHHFSLDIDIGCTDLHENLGVWV 898

Qy	998	VFKIKTQEGHARLGNLFIEIEKPLLGALSVRKGAEKWRDKREKLOLETKRVVTEAKEA	957
Db	999	VFKIKTQEGHARLGNLFIEIEKPLLGALSVRKGAEKWRDKREKLOLETKRVVTEAKEA	958
Qy	958	VDALFVDSQYNRLQADTNIGIMHAADKLVRHIREAYLSELSEVIPGVNAEIPFEELEGRPIIT	1017
Db	959	VDALFVDSQYDQLQADTNIGIMHAADKLVRHIREAYLSELSEVIPGVNAEIPFEELEGHIIIT	1018
Qy	1018	AISLYDARNVVKNGDFNGLACMNVKGHDVQQSHRSVLVIPPEWAEVSQAVRVCFGRG	1077
Db	1019	AMSLYDARNVVKNGDFNGLTGMNVKGHDVQQSHRSDLVIPPEWAEVSQAVRVCFGRG	1078
Qy	1078	YLIRVTAYKEGYGEGCVTIIEIENNTDELAFKNCBEEBVEVPTDTGTCDNTYHQGTAVCN	1137
Db	1079	YLIRVTAYKEGYGEGCVTIIEIENNTDELAFKNCBEEBVEVPTDTGTCDNTYHQGTAACN	1138
Qy	1138	SRNAGYEDAYEVDVTASVNVKPYEETTYTDVRDNDHCEYDRGVNVPPDPAGVMTKELE	1197
Db	1139	SRNAGYEDAYEVDVTASVNVKPYEETTYTDVRDNDHCEYDRGVNVPPDPAGVVTKELE	1198
Qy	1198	YFPETDKVWIEIGBTEGKFIVDSVELLMEE	1228
Db	1199	YFPETDVTWIEIGBTEGKFIVDSVELLMEE	1229

RESULT 6

ID CIBD_BACTZ STANDARD; PRT; 1231 AA.
 AC Q9ZAS5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Pesticidal crystal protein cryIBD (Insecticidal delta-endotoxin
 DE CryIb(d)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
 GN Names-cryIBD; Synonyms-cryIB(d), cryIa1, cryE1;
 GN Bacillus thuringiensis (subsp. wuhanensis).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=52024;
 CC [1] RN
 CC SEQUENCE FROM N.A.
 CC STRAIN=HD-525;
 CC MEDLINE=20153386; PubMed=10688690;
 CC Kuo W.-S., Lin J.-H., Tseng C.-C., Kao S.-S., Chak K.-P.;
 CC "Cloning of two new cry genes from *Bacillus thuringiensis* subsp.
 CC *wuhanensis* strain.";
 CC Curr. Microbiol. 40:227-232(2000).
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
 CC epithelial cells of lepidopteran larvae. Toxic to *Plutella*
 CC *xylostella*.
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 CC terminus.
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.
 CC -----
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 CC ential entities requires a license agreement (See <http://www.isb-sib.ch/announ>-
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U70726; AAD10292.1; -;
 CC HSSP; P02965; 1CIY.
 CC InterPro; IPR001178; Endotoxin.
 CC InterPro; IPR005638; Endotoxin_C.
 CC InterPro; IPR005639; Endotoxin_N.
 CC InterPro; IPR008979; Gal_bind_Like.
 CC Pfam; PF03944; Endotoxin_C; 1.
 CC Pfam; PF00555; Endotoxin_W; 1.
 CC Pfam; PF03945; Endotoxin_N; 1.

Db 954 YTEAKETVDALFVDSHYNRLQADTNIGMTHAADRLVHRHIEAYLPPELPFGINAVIFEE 1013
QY 1011 LEGRIITAIISLYDARNVVKNGDFNGLACWNVKGHVQVQSHRSVVLVPIPEAEVSQAV 1070
Db 1014 LENRISTAFSLYDARNVVKNGDFNGLACWNVKGHVQVQSHRSVVLVPIPEAEVSQAV 1073
QY 1071 RVCGRGYILRVATYKGGYGGCVTIHEIENNTDELKFKNCEEEVYPTDGTCDNYTAH 1130
Db 1074 RVCGRGYILRVATYKGGYGGCVTIHEIENNTDELKFKNCEEEVYPTDGTCDNYTAH 1133
QY 1131 OCTAVCNENAGYDAEYVDVTASVNYKPYEETVYDVRDNHCEYDRGYNYPPLPAG 1190
Db 1134 QGTAAACNRNAGYDAEYVDVTASVNYKPYEETVYDVRDNHCEYDRGYNYPPLPAG 1193
QY 1191 YMTKELEYPPETDKVWIEIGETEGKFIVDSVELLMEE 1228
Db 1194 YVTKELSYFPETDVTWIEIGETEGKFIVDSVELLMEE 1231

RESULT 7
Q8KNY2 PRELIMINARY; PRT; 1231 AA.
AC Q8KNY2;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE CryIBII.
GN Name=CryIBII;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Isakov I.A., Isakov Y.B., Rymar' S.E., Varovoi S.V.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF138457; AA093496.1; -;
DR HSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin.C.
DR InterPro; IPR005639; endotoxin.N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1-
DR Pfam; PF00555; Endotoxin_N; 1-
DR Pfam; PF03945; Endotoxin_N; 1-
SQ SEQUENCE 1231 AA; 139764 MW; C9F2848A9297EA00 CRC64;

Query Match 80.1%; Score 5188.5; DB 2; Length 1231;
Best Local Similarity 79.3%; Pred. No. 9e-318;
Matches 982; Conservative 97; Mismatches 142; Indels 17; Gaps 9;

QY 1 LTSNRKNEIINALSIPAVNSHSTOMDLSPARIEDSLCAEAGNINPLVSASTVQTGI 60
Db 1 MTSNRKNEIINALSIPVSNPSTQMNLSPARIEDSLCAEAGNINPLVSASTVQTGI 60
QY 61 NIAGILGVLPFAGQATASFSFLVGLWLPGRDOWEIEFLHVEQLINQITENARNTA 120
Db 61 NIAGILGVLPFAGQATASFSFLVGLWLPGRDOWEIEFLHVEQLINQITENARNTA 120
QY 121 LARLOGLGDSFRAYQOQSLMEDLENRDARTSVLTQVIALELDFPLNAMPLFAIRNQSV 180
Db 121 IARLEGLGRYSYQQALETWLDNRDARSRIILERYVALELDITTAIPFIRINEVP 180
QY 181 LMVYAQANLHLLRLDASLPGSFGLTSQBIQRYRQVEQTRDYSYCVWYNTGLN 240
Db 181 LMVYAQANLHLLRLDASLPGSFGLTSQBIQRYRQVEQTRDYSYCVWYNTGLN 240
QY 241 SIRGNTAAWRYNQRFRDLTLGLVLDLVALPSYDTRTYPINTSAQLTREVYTDAGTG 300
Db 241 NLRGNTAAWRYNQRFRDLTLGLVLDLVALPSYDTRTYPINTSAQLTREVYTDAGTG 300

QY 301 V--NMASMNWYNNAPSPSAIETAVIRSPHLLDFLEQLTIPTSTSRSGATRHMTYWRGHT 358
Db 301 APSGFASTWNNNAPSPSAIEAALFRPHLLDPPEQLTIYSASSRWSSTQHMNVVGH 360
QY 359 IQSRPIGGGLNTSTHGST-NTSINPVLRSFPDRDYVWYTESVAGVLLMGIYLEPIHGVPTV 417
Db 361 LNFPIGGTLNTSTQGLTNNTSINPVLQFTSRDYRTESNAGTNI--LFTTVNAGVPM 418
QY 418 RFPNPNQNTPERGTANYSQPVESGLQDKDSELPPEPPERPNYVESYHSLSHIGLIS 477
Db 419 RFPNPNQNTPERGTANYSQPVESGLQDKDSELPPEPPERPNYVESYHSLSHIGLIS 478
QY 478 QSRVHPVYVSWTHRSADRTNTISSDITQIPLVKSFNLSGTSVVGSGFTGDDIIRTN- 536
Db 479 GNTLRAPVYVSWTHRSADRTNTIGPNRITQIPAVKGRPLFNG-SVTSFGFTGDDVRLNR 537
QY 537 VNGSVLSMG-----LNFNNTSLQRYRVRVRAAQTVMVLRVTVGSGSTTFDQGFPTMGN 591
Db 538 NNGNIQNRGYIEVPIQFTSTS-TRYRVRVRVAVSTSIELNVNLGNSSIFTTLPTAASL 596
QY 592 ESLTSQSPPRAEPFVGI--SASSGQTAGISINNAGROTFFHDKIEFIPITATFEAEYDLE 650
Db 597 DNLQSGDFGYEINNAFTSATGNIVGARNFSANA---EVIIDRFEFIPVTATFEAEYDLE 653
QY 651 RAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDDFCLDEKRELLKVKYAKRLS 710
Db 654 RAQAVNALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDDFCLDEKRELLKVKYAKRLS 713
QY 711 DERMLLQDPNPTSINKQDPFITSTNEQSNFTSIHQSEHGHWGSGENITTOEGNDVPEKNYV 770
Db 714 DERMLLQDPNFTFISGQLSFASIDQSNFTSINELSEHGHWGSGENITTOEGNDVPEKNYV 773
QY 771 TLRGTENECPYLYQKIGESLKAITYQLRGYIEDSQDLLEIYLIRYNKHEHETLDVPGT 830
Db 774 TLRGTENECPYLYQKIGESLKAITYQLRGYIEDSQDLLEIYLIRYNKHEHETLDVPGT 833
QY 831 ESMVPLSVESPIGRGEPNRCAPHFENWPDLDSCRDGECARHSHHSHFTLDDVGCCTDLH 890
Db 834 DSLWPLSVKSPIGRCGEPNRCAPHFENWPDLDSCRDGECARHSHHSHFTLDDVGCCTDLH 893
QY 891 ENLGVWVVFJKITQEGHARLGNLSEPIESKPLLGALSRVKAERKWRDKREKLETKRV 950
Db 894 ENLGVWVVFJKITQEGHARLGNLSEPIESKPLLGALSRVKAERKWRDKREKLETKRV 953
QY 951 YTEAKEAVDALFVDSQYVNLQADTNIGMTHAADRLVHRHIEAYLPPELPFGINAVIFEE 1010
Db 954 YTEAKEAVDALFVDSQYVNLQADTNIGMTHAADRLVHRHIEAYLPPELPFGINAVIFEE 1013
QY 1011 LEGRIITAIISLYDARNVVKNGDFNGLACWNVKGHVQVQSHRSVVLVPIPEAEVSQAV 1070
Db 1014 LENRISTAFSLYDARNVVKNGDFNGLACWNVKGHVQVQSHRSVVLVPIPEAEVSQAV 1073
QY 1071 RVCGRGYILRVATYKGGYGGCVTIHEIENNTDELKFKNCEEEVYPTDGTCDNYTAH 1130
Db 1074 RVCGRGYILRVATYKGGYGGCVTIHEIENNTDELKFKNCEEEVYPTDGTCDNYTAH 1133
QY 1131 QGTAVCNENAGYDAEYVDVTASVNYKPYEETVYDVRDNHCEYDRGYNYPPLPAG 1190
Db 1134 QGTAAACNRNAGYDAEYVDVTASVNYKPYEETVYDVRDNHCEYDRGYNYPPLPAG 1193
QY 1191 YMTKELEYPPETDKVWIEIGETEGKFIVDSVELLMEE 1228
Db 1194 YVTKELSYFPETDVTWIEIGETEGKFIVDSVELLMEE 1231

RESULT 8
C1BC_BACTM
ID C1BC_BACTM STANDARD; PRT; 1233 AA.
AC Q45774;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin)


```
Db 1 MTSNRKNEIINALSIPAVSNHSAQNNLSTDAIEDSLCIAEGNNIDPFVSASTVQTGI 60
QY 61 NIAGRIILGVLPFAGQIASFYSFLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
Db 61 NIAGRIILGVLPFAGQIASFYSFLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
QY 121 LARLOGLGDSFRAYQOGLSEDLWENRDARTSRVLTQVIALELDFLNAMPLFAIRNQVVP 180
Db 121 LARLOGLGDSFRAYQOGLSEDLWENRDARTSRVLTQVIALELDFLNAMPLFAIRNQVVP 180
QY 181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVVWNTGLN 240
Db 181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVVWNTGLN 240
QY 241 SLRGTAASWRYNQFRDLTLGLVDLVALFSDYDTRYPINTSAQLTREYVTDIGRTN 300
Db 241 SLRGTAASWRYNQFRDLTLGLVDLVALFSDYDTRYPINTSAQLTREYVTDIGRTN 300
QY 301 V--NWASMNWYNNAPSPSAIETAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHT 358
Db 301 V--NWASMNWYNNAPSPSAIETAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHT 358
QY 359 IQSRPIGGLNTSTHGTNTSINPVRLSPFSDVYVWTSYAGVLLWGLYLPBPIHGVPVTR 418
Db 359 IQSRPIGGLNTSTHGTNTSINPVRLSPFSDVYVWTSYAGVLLWGLYLPBPIHGVPVTR 418
QY 418 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVSGPGFTGDDIIRTNVN 537
Db 418 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVSGPGFTGDDIIRTNVN 537
QY 539 GSLSMGLNFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQS 598
Db 539 GSLSMGLNFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQS 598
QY 598 FRFAEPFVGISASGSGTAGISINNAGQTFHDKIEPIPIATPEAYDYDLERAQEAUNA 658
Db 598 FRFAEPFVGISASGSGTAGISINNAGQTFHDKIEPIPIATPEAYDYDLERAQEAUNA 658
QY 658 LFTNTNPRRLKTGVDYHIDVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 717
Db 658 LFTNTNPRRLKTGVDYHIDVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 717
QY 719 PNFTSINKQPDFISTNEQSNFTSIHQSEHGWSGSENIITIQEGNDVPKENVYVTLPGTFNE 778
Db 719 PNFTSINKQPDFISTNEQSNFTSIHQSEHGWSGSENIITIQEGNDVPKENVYVTLPGTFNE 778
QY 778 CYPTLYQKIGSELKAYTRYQLSGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWLSV 838
Db 778 CYPTLYQKIGSELKAYTRYQLSGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWLSV 838
QY 839 ESPIGRCGCEP NR 850
Db 839 ESPIGRCGCEP NR 849
```

RESULT 12

```
AA593797
ID AA593797 PRELIMINARY; PRT; 849 AA.
AC AA593797;
DT 26-APR-2004 (TReMBLrel. 27, Created)
DT 26-APR-2004 (TReMBLrel. 27, Last sequence update)
DT 26-APR-2004 (TReMBLrel. 27, Last annotation update)
DE Cry1B type crystal protein (Fragment).
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group; Bacillus thuringiensis.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=K1;
RA Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;
RT "cry1B";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570734; AAS93797.1; -.
FT NON TER 849
SQ SEQUENCE 849 AA; 95886 MW; PCB98495787CF763 CRC64;
```

Query Match

Best Local Similarity 60.2%; Score 3901.5; DB 2; Length 849;
Matches 756; Conservative 33; Mismatches 58; Indels 5; Gaps 3;

```
QY 1 MTSNRKNEIINALSIPAVSNHSAQNNLSTDAIEDSLCIAEGNNIDPFVSASTVQTGI 60
Db 1 MTSNRKNEIINALSIPAVSNHSAQNNLSTDAIEDSLCIAEGNNIDPFVSASTVQTGI 60
QY 61 NIAGRIILGVLPFAGQIASFYSFLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
Db 61 NIAGRIILGVLPFAGQIASFYSFLVGLWPRGRDQWEIFLEHVQLINQOITENARNTA 120
QY 121 LARLOGLGDSFRAYQOGLSEDLWENRDARTSRVLTQVIALELDFLNAMPLFAIRNQVVP 180
Db 121 LARLOGLGDSFRAYQOGLSEDLWENRDARTSRVLTQVIALELDFLNAMPLFAIRNQVVP 180
QY 181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVVWNTGLN 240
Db 181 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVVWNTGLN 240
QY 241 SLRGTAASWRYNQFRDLTLGLVDLVALFSDYDTRYPINTSAQLTREYVTDIGRTN 300
Db 241 SLRGTAASWRYNQFRDLTLGLVDLVALFSDYDTRYPINTSAQLTREYVTDIGRTN 300
QY 301 V--NWASMNWYNNAPSPSAIETAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHT 358
Db 301 V--NWASMNWYNNAPSPSAIETAVIRSPHLLDFLEQLTIFSTSRWSATRHMTYWRGHT 358
QY 359 IQSRPIGGLNTSTHGTNTSINPVRLSPFSDVYVWTSYAGVLLWGLYLPBPIHGVPVTR 418
Db 359 IQSRPIGGLNTSTHGTNTSINPVRLSPFSDVYVWTSYAGVLLWGLYLPBPIHGVPVTR 418
QY 418 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVSGPGFTGDDIIRTNVN 537
Db 418 NTLRAPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVSGPGFTGDDIIRTNVN 537
QY 539 GSLSMGLNFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQS 598
Db 539 GSLSMGLNFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQS 598
QY 598 FRFAEPFVGISASGSGTAGISINNAGQTFHDKIEPIPIATPEAYDYDLERAQEAUNA 658
Db 598 FRFAEPFVGISASGSGTAGISINNAGQTFHDKIEPIPIATPEAYDYDLERAQEAUNA 658
QY 658 LFTNTNPRRLKTGVDYHIDVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 717
Db 658 LFTNTNPRRLKTGVDYHIDVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQD 717
QY 719 PNFTSINKQPDFISTNEQSNFTSIHQSEHGWSGSENIITIQEGNDVPKENVYVTLPGTFNE 778
Db 719 PNFTSINKQPDFISTNEQSNFTSIHQSEHGWSGSENIITIQEGNDVPKENVYVTLPGTFNE 778
QY 778 CYPTLYQKIGSELKAYTRYQLSGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWLSV 838
Db 778 CYPTLYQKIGSELKAYTRYQLSGYIEDSDQLEIYLIRYNAKHETLDVPGTESVWLSV 838
QY 839 ESPIGRCGCEP NR 850
Db 839 ESPIGRCGCEP NR 849
```

RESULT 13

ID C1CB_BACTG STANDARD; PRT; 1176 AA.
 AC P56953;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Pepticidial crystal protein cryIcB (Insecticidal delta-endotoxin
 GN Name=cryIcB; (Crystalline entomocidal protoxin) (133 kDa crystal protein).
 OS Bacillus thuringiensis-cryIc(b);
 OC Bacillus thuringiensis (subsp. galleriae).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=29338;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-29.
 RX MEDLINE=93236401; PubMed=8476286;
 RA Kalman S.S.;
 RT "Cloning a novel cryIC-type gene from a strain of Bacillus
 thuringiensis galleriae";
 RL Appl. Environ. Microbiol. 59:1131-1137(1993)
 CC -|- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
 epithelial cells of insects. Toxic to Spodoptera exigua and
 Trichoplusia ni.
 CC -|- DEVELOPMENTAL STAGE: The crystal protein is produced during
 sporulation and is accumulated both as an inclusion and as part of
 the spore coat.
 CC -|- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 terminus.
 CC -|- SIMILARITY: Belongs to the delta endotoxin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M97880; -; NOT_ANNOTATED_CDS.
 DR PIR; A48970; A48970.
 DR HSSP; P02965; 1CIY.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin C.
 DR InterPro; IPR005639; endotoxin N.
 DR InterPro; IPR008979; Gal bind like.
 DR Pfam; PF03944; Endotoxin C; 1.
 DR Pfam; PF00555; Endotoxin M; 1.
 DR Pfam; PF03945; Endotoxin N; 1.
 KW Sporulation; Toxin.
 SQ SEQUENCE 1176 AA; 132867 MW; 108233494C2AC018 CRC64;

Query Match 58.5%; Score 3791; DB 1; Length 1176;
 Best Local Similarity 62.3%; Pred. No. 9.6e-230;
 Matches 762; Conservative 125; Mismatches 241; Indels 96; Gaps 16;

QY 40 C1AEGNNINLVASSTVQTG---INIAGRILGVL---GVFPAQIASFVSFLVGLWPRG 93
 DB 14 CLSPPEEL--LDGERISTGSSIDISLSVLQVLSNFFVGGFLVGLLDFVNGIVGP-- 69
 QY 94 RDWEIEFLEHVEQLNQIITENARTALRQLGLGDSFRAYQOSLEDWLENRDDARTSV 153
 DB 70 -SPWDAFLVQLQLINERIAAYARSAAISNLEGLGNFNFIYFAFKEWADPDNPVTR 128
 QY 154 LYTYOYIALEDLFLNAPLFAIRNOQVPLLMVYQAANLHLLLRDASLFGSFGLTQSRI 213
 DB 129 VVDRIFLDGLLERDIFSFRIAGFEVPLLSVYQAANLHLLLRDSSIFGARWGLTTNV 188
 QY 214 QRYERQVEQTRDYSYCVWYNTGLNSLGTNAASWVRNQFRDRLTGLVLDVALFPS 273
 DB 189 NENYNRLIRHIDEVANHCAADYNGRLNPLKSTYQDMITYNRRLDRLTLTVLDIAFPFS 248
 QY 274 YDTRTPINTSAQLTREVYTDAGTGVANMAMNWNNNNAPSFAIETAVIRSPHLLDPL 333

Db 249 YDNRYPISQVGQLTREIYTDPLITFNPQLQSV---AQLPTFNVMESNAIRTPHLPDVL 304
 QY 334 BQLTIFSTSRWSATRHMTYWRGHTIQSRPIGGGLNTSTHGSLTNTSINPVLRSFFSRDVI 393
 Db 305 NNLTIPTD--WFSVGRNFYWGGRVTSNRIGGNITSPYIGREANQEPSPRSFTFNGPVF 361
 QY 394 WTESYAGVLLWGIYLBPIHGVPIVR-----FN-----FRNPONTFE---RGT 432
 Db 362 RTLSN-----PTFRPLQOPWPAPPFNFLRGVEGFESTPLNSFTYRGRGT 405
 QY 433 ANYSQPYESPGLOKDSLETPEPETERPNYESYSHRLSHIGLISQSRVHV---PVYSW 488
 Db 406 V-----DSLTELPEPDSVPREGYSHRLCHATFVQSGTPTFLTGTGVFSW 451
 QY 489 THRSADRTNTISSDSITQPLVKSFNLSNGTSVVGPGFTGGDIIRTNVNGSVLSMGLNF 548
 Db 452 THRSATDRNIYDPVINQIPLVKAFLNTSGTSVVRGPGFTGGDIIRTNVNGSVLSMGLNF 511
 QY 549 NNTSLQRYRVRYAASQTMWLRTVVGSTTTDQGPSTMSANESITQSOFPAEPFVCI 608
 Db 512 SNTTLQRYRVRYAASQTMWSTVVGSTTGNQGFPSMSANGALTSQSFAPFPPVGI 571
 QY 609 SASGSGTAGISNNAGROTTFHDKIEFIPITATPEAEYDLERAQEAVALFTNTPRRL 668
 Db 572 SASGSGAGISISNNVGRQMFHLDRIEFLPTVSTFEERYDLERAQEAVALFTNQLGL 631
 QY 669 KTDVTDYHIDQVSNLVACLSDEFCLDERKLEKVKYAKELSDERNLLODPNFTSINKQP 728
 Db 632 KTDVTDYHIDQVSNLVECLSDDEFCLDERKLEKVKYAKELSDERNLLODRNFRSINGQL 691
 QY 729 DFISTNEQNFSTSIHQSHGWSGSENITIQEGNDVFKENYVTLPGTNECVPTLYOKI 788
 Db 692 D-----RGWRGSTDITIQGGDVFKENYVTLPGTDECVPTLYOKI 733
 QY 789 GESELKAYTRYOLRGVIEDSOOLEYLRYNKAKHETLDVPGTESVWPLSVSPICRCQEP 848
 Db 734 DESKLSYTRYELRGYIEDSOOLEYLRYNKAKHEIVNVPGTGSLWPLSISNSIGPCGEP 793
 QY 849 NRCAPHFEMNPDLDCSCRDGEKCAHSHHFSLDIDIGCTDLHENLGVWVFKITQEGHA 908
 Db 794 NRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLGWVWIFKITQDQHA 853
 QY 909 RLGNLEFEEKPLLEALSRVKRAEKWRDKREKQLQLETRKRVYTEAKEAVDALFVDSQYN 968
 Db 854 RLGNLEFEEKPLLEALSRVKRAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQYD 913
 QY 969 RLQADTNIGMIHAADKLVRIRIYREALYLSLSVPGVNAEIPFEELEGRITITSLYDARNV 1028
 Db 914 RLQADTNIAHIAADKVRIRIYREALYLPESLVPVNAIGIPEELEGRIFTAYSLYDARNVI 973
 QY 1029 KNGDFNGLACWNKGVHDV--QSHHRSVLVPEWEAEVSQAVRCVPGRGYILRVATYKE 1087
 Db 974 KNGDFNGLLCLWNLKGVHDVEEQNNHRSVLVPEWEAEVSQAVRCVPGRGYILRVATYKE 1033
 QY 1088 GYGEGCVTHIEINNTDELKFNCEEEVPTDTGTCNDYTAHQ---GTAVCHSRNAGYE 1144
 Db 1034 GYGEGCVTHIEINNTDELKFNCEEEVPTDTGTCNDYTAHQ---GTAVCHSRNAGYE 1092
 QY 1145 DAYEVDTTASVNYKPTVEEETTDVDRDNHCEYDRGVVYPPPLPAGYMTKELEYFPETDK 1204
 Db 1093 KSYESNSSVQADYASVYEEKADTDGRDRDNHCEYDRGVVYPPPLPAGYMTKELEYFPETDK 1152
 QY 1205 VWIEIGTEGKFIIVDSVELLIMEE 1228
 Db 1153 VWIEIGTEGTFIVDSVELLIMEE 1176

RESULT 14
 C1JB_BACTU
 ID C1JB_BACTU
 AC Q45716;
 DT 30-MAY-2000 (Rel. 39, Created)

